from the chromosome via a second recombination event over the duplicated target gene sequence either completed the allelic exchange or reconstituted the wild-type genotype. Subsequent loss of the plasmid in the absence of antibiotic selection pressure resulted in an erythromycin-sensitive phenotype. In order to assess gene replacement a screening of erythromycin-sensitive colonies was performed by analysis of the target gene PCR amplicons.

FIGURE 7 reports a schematic of the IS-1 operon for each knock-out strain generated, along with the deletion position within the amino acidic sequence. Most data presented here concern the COH1 deletion strains, in which the expression of each of the antigens is higher by DNA microarray analysis (data not shown) as well as detectable by FACS analysis (see FIGURE 8). The double mutant in 2603 Δ80, Δ104 double mutant was constructed by sequential allelic exchanges of the shown alleles.

Immunization protocol

Immune sera for FACS experiments were obtained as follows.

Groups of 4 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were immunized with the selected GBS antigens, (20 μg of each recombinant GBS antigen), suspended in 100 μl of PBS. Each group received 3 doses at days 0, 21 and 35. Immunization was performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. In each immunization scheme negative and positive control groups are used. Immune response was monitored by using serum samples taken on day 0 and 49.

FACS analysis

Preparation of paraformaldehyde treated GBS cells and their FACS analysis were carried out as follows.

GBS serotype COH1 strain cells were grown in Todd Hewitt Broth (THB; Difco Laboratories, Detroit, Mich.) to OD600nm = 0.5. The culture was centrifuged for 20 minutes at 5000 rpm and bacteria were washed once with PBS, resuspended in PBS containing 0.05% paraformaldehyde, and incubated for 1 hours at 37 °C and then overnight at 4°C. 50μl of fixed bacteria (OD600 0.1) were washed once with PBS, resuspended in 20μl of Newborn Calf Serum, (Sigma) and incubated for 20 min. at room temperature. The cells were then incubated for 1 hour at 4°C in 100μl of preimmune or immune sera, diluted 1:200 in dilution buffer (PBS, 20% Newborn Calf Serum, 0.1% BSA). After centrifugation and washing with 200μl of washing buffer (0.1% BSA in PBS), samples were incubated for 1 hour at 4°C with 50μl of R-Phicoerytrin conjugated F(ab)2 goat anti-mouse IgG (Jackson ImmunoResearch Laboratories; Inc.), diluted 1:100 in dilution buffer. Cells were washed with 200μl of washing buffer and resuspended in 200μl of PBS. Samples were analysed using a FACS Calibur apparatus (Becton Dickinson, Mountain View, Calf.) and data were analyzed using the Cell Quest Software (Becton Dickinson). A shift in mean fluorescence intensity of > 75 channels compared to preimmune sera from the same mice was considered positive. This cutoff

was determined from the mean plus two standard deviations of shifts obtained with control sera raised against mock purified recombinant proteins from cultures of *E. coli* carrying the empty expression vector and included in every experiment. Artifacts due to bacterial lysis were excluded using antisera raised against 6 different known cytoplasmic proteins all of which were negative

FACS data on COH1 single KO mutants for GBS 104 and GBS 80 indicated that GBS 80 is required for surface localization of GBS 104.

As shown in FIGURE 8, GBS 104 is not surface exposed in the Δ80 strain (second column, bottom), but is present in the whole protein extracts (see FIGURE 10). Mean shift values suggest that GBS 104 is partially responsible for GBS 80 surface exposure (Mean shift of GBS 80 is reduced to ~60% wild-type levels in Δ104), and that GBS 80 is over-expressed in the complemented strain (mean shift value ~200% wild-type level). The Δ80/pGBS 80 strain contains the GBS 80 orf cloned in the shuttle-vector pAM401 (Wirth, R., F. Y. An, et al. (1986). J Bacteriol 165(3): 831-6). The vector alone does not alter the secretion pattern of GBS 104 (right column). FACS was performed on mid-log fixed bacteria with mouse polyclonal antibodies as indicated at left. Black peak is pre-immune sera, colored peaks are sera from immunized animals.

EXAMPLE 3: Deletion of GBS 80 causes attenuation *in vivo*.

This example demonstrates that deletion of GBS 80 causes attenuation *in vivo*, suggesting that this protein contributes to bacterial virulence.

By using a mouse animal model, we studied the role of GBS 80 and GBS 104 in the virulence of S. agalactiae.

Groups of ten outbred female mice 5-6 week weeks old (Charles River Laboratories, Calco Italy) were inoculated intraperitoneally with different dilutions of the mutant strains and LD50 (lethal dose 50) were calculated according to the method of Reed and Muench [Reed, L. J. and H. Muench (1938).The American Journal of Hygiene 27(3): 493-7]. As presented in the table below the number of colony forming units (cfu) counted for both the Δ80 and the Δ80, Δ104 double mutants is about 10 fold higher when compared to the wild type strain suggesting that inactivation of GBS 80 but not GBS 104 is responsible for an attenuation in virulence. This finding indicates that GBS 80 gene in the AI-1 might contribute to virulence.

Table Lethal dose 50% analysis of AI-1 mutants in the 2603 strain background. LD50s were performed by IP injection of female CD1 mice at an age of 5-6 weeks. LD50s were calculated by the method of Reed and Muench (8).

GBS strain	LD_{50}, cfu	Number of Experiments
Wild Type 2603	2×10^8	4
Δ104 mutant	$\sim 2 \times 10^8$	1
Δ80 mutant	2.6×10^9	3
Δ80, Δ104 double mutant	$\sim 2 \times 10^9$	1

EXAMPLE 4: Effect of Adhesin Island Sortase Deletions on Surface Antigen Presentation

This example demonstrates the effect of adhesin island sortase deletions on surface antigen presentation.

FACS analysis results set forth in FIGURE 9 show that a deletion in sortase SAG0648 prevented GBS 104 from reaching the surface and slightly reduced the surface exposure of GBS 80 (fourth panel; mean shift value ~60% wild-type COH1). In the double sortase knock-out strain, neither antigen was surface exposed (far right panel). Either sortase alone was sufficient for GBS 80 to arrive at the bacterial surface (third and fourth columns, top). No effect was seen on surface exposure of antigens GBS 80 or GBS 104 in the ΔGBS 52 strain. Antibodies derived from purified GBS 52 were either non-specific or were FACS negative for GBS 52 (data not shown). FACS analysis was performed as described above (see EXAMPLE 2).

As shown in FIGURE 10, inactivation of GBS 80 has no effect on GBS 104 expression as much as GBS 104 knock out doesn't change the total amount GBS 80 expressed. The Western blot of whole protein extracts (strains noted above lanes) probed with anti-GBS 80 antisera is shown in panel A. Arrow indicates expected size of GBS 80 (60 kDa). GBS 80 antibodies recognize a doublet, the lower band is not present in ΔGBS 80 strains. Panel B shows a Western blot of whole protein extracts probed with anti-GBS 104 antisera. Arrow indicates expected size of GBS 104 (99.4 kDa). Protein extracts were prepared from the same bacterial cultures used for FACS (FIGURES 8 and 9). In conclusion, although GBS 104 does not arrive at the surface in the Δ80 strain by FACS (FIGURE 8, second column), it is present at approximately wild-type levels in the whole protein preps (B, second lane). Approximately 20 μg of each protein extract was loaded per lane.

Western-blot analysis

Aliquots of total protein extract mixed with SDS loading buffer (1x: 60 mM TRIS-HCl pH 6.8, 5% w/v SDS, 10% v/v glycerin, 0.1% Bromophenol Blue, 100 mM DTT) and boiled 5 minutes at 95° C, were loaded on a 12.5% SDS-PAGE precast gel (Biorad). The gel is run using a SDS-PAGE running buffer containing 250 mM TRIS, 2.5 mM Glycine and 0.1 %SDS. The gel is electroblotted onto nitrocellulose membrane at 200 mA for 60 minutes. The membrane is blocked for 60 minutes with PBS/0.05 % Tween-20 (Sigma), 10% skimmed milk powder and incubated O/N at 4° C with PBS/0.05 % Tween 20, 1% skimmed milk powder, with the appropriate dilution of the sera. After washing twice with PBS/0.05 % Tween, the membrane is incubated for 2 hours with peroxidase-conjugated secondary anti-mouse antibody (Amersham) diluted 1:4000. The nitrocellulose is washed three times for 10 minutes with PBS/0.05 % Tween and once with PBS and thereafter developed by Opti-4CN Substrate Kit (Biorad).

Example 5: Binding of Adhesin Island proteins to epithelial cells and effect of Adhesin Island proteins on capacity of GBS to adhere to epithelial cells.

This example illustrates the binding of AI proteins to epithelial cells and the effect of AI proteins on the capacity of GBS to adhere to epithelial cells.

Applicants analysed whether recombinant AI surface proteins GBS 80 or GBS 104 would demonstrate binding to various epithelial cells in a FACS analysis. Applicants also analysed whether

deletion of AI surface proteins GBS 80 or GBS 104 would effect the capacity of GBS to adhere to and invade ME180 cervical epithelial cells.

As shown in Figure 28, deletion of GBS 80 sequence from GBS strain isolate 2603 (serotype V) did not affect the capacity of the mutated GBS to adhere to and invade ME180 cervical epithelial cells. Here ME180 cervical carcinoma epithelial cells were infected with wild type GBS 2603 or GBS 2603 Δ80 isogenic mutant. After two hours of infection, non-adherent bacteria were washed off and infection prolonged for a further two hours and four hours. In invasion experiments, after each time point, was followed by a two hour antibiotic treatment. Cells were then lysed with 1% saponin and lysates platedon TSA plates. As shown in Figure 28, there was little difference between the percent invasion or percent adhesion of wild type and mutant strains up to the four hour time point.

Figure 30 repeats this experiment with both Δ104 and Δ 80 mutants from a different strain isolate. Here, ME180 cervical carcinoma epithelial cells were infected with GBS strain isolate COH (serotype III) wild type or COH1 ΔGBS 104 or COH1 Δ80 isogenic mutant. After one hour of infection, non-adherent bacteria were washed off and the cells were lysed with 1% saponin. The lysates were plated on TSA plates. As shown in Figure 30, while there was little difference in the percent invasion, there was a significant decrease in the percent association of the Δ104 mutant compared to both the wild type and Δ80 mutant.

The affect of AI surface proteins on the ability of GBS to translocate through an epithelial monolayer was also analysed. As shown in Figure 31, a GBS 80 knockout mutant strain partially loses the ability to translocate through an epithelial monolayer. Here epithelial monolayers were inoculated with wildtype or knockout mutant in the apical chamber of a transwell system for two hours and then non-adherent bacteria were washed off. Infection was prolonged for a further two and four hours. Samples were taken from the media of the basolateral side and the number of colony forming unties measured. Transepithelial electrical resistance measured prior to and after infection gave comparable values, indicating the maintenance of the integrity of the monolayer. By the six hour time point, the Δ80 mutants demonstrated a reduced percent transcytosis.

A similar experiment was conducted with GBS 104 knock out mutants. Here, as shown in Figure 22, the Δ104 mutants also demonstrated a reduced percent transcytosis, indicating that the mutant strains translocate through an epithelial monolayer less efficiently than their isogenic wild type counterparts.

Applicants also studied the effect of AI proteins on the capacity of a GBS strain to invade J774 macrophage-like cells. Here, J774 cells were infected with GBS COH1 wild type or COH1 ΔGBS104 or COH1 ΔGBS80 isogenic mutants. After one hour of infection, non-adherent bacteria were washed off and intracellular bacteria were recovered at two, four and six hours post antibiotic treatment. At each time point, cells were lysed with 0.25% Triton X-100 and lysates plated on TSA plates. As shown in Figure 32, the Δ104 mutant demonstrated a significantly reduced percent invasion compared to both the wild type and Δ80 mutant.

Example 6: Hyperoligomeric structures comprising AI surface proteins GBS 80 and GBS 104.

This example illustrates hyperoligomeric structures comprising AI surface proteins GBS 80 and GBS 104. A GBS isolate COH1 (serotype III) was adapted to increase expression of GBS 80. Figure 34 presents a regular negative stain electron micrograph of this mutant; no pilus or hyperoligomeric structures are distinguishable on the surface of the bacteria. When the EM stain is based on anti-GBS 80 antibodies labelled with 10 or 20 nm gold particles, the presence of GBS 80 throughout the hyperoligomeric structure is clearly indicated (Figures 36, 37 and 38). EM staining against GBS 104 (anti-GBS 104 antibodies labelled with 10 nm gold particles) also reveals the presence of GBS 104 primarily on or near the surface of the bacteria or potentially associated with bacterial peptidoglycans (Figure 39). Analysis of this same strain (over-expressing GBS 80) with a combination of both anti-GBS 80 (using 20 nm gold particles) and anti-GBS 104 (using 10 nm gold particles) reveals the presence of GBS 104 on the surface and within the hyperoligomeric structures (see Figures 40 and 41).

Example 7: GBS 80 is necessary for polymer formation and GBS 104 and sortase SAG0648 are necessary for efficient pili assembly

This example demonstrates that GBS 80 is necessary for formation of polymers and that GBS 104 and sortase SAG0648 are necessary for efficient pili assembly. GBS 80 and GBS 104 polymeric assembly was systematically analyzed in Coh1 strain single knock out mutants of each of the relevant coding genes in AI-1 (GBS 80, GBS 104, GBS 52, sag0647, and sag0648). Figure 41 provides Western blots of total protein extracts (strains noted above lanes) probed with either anti-GBS 80 (left panel) sera or anti-GBS 104 sera (right panel) for each of these Coh1 and Coh1 knock out strains. (Coh1, wild type Coh1; Δ80, Coh1 with GBS 80 knocked out; Δ104, Coh1 with GBS 104 knocked out; Δ52, Coh1 with GBS 52 knocked out; Δ647, Coh1 with SAG0647 knocked out; Δ648, Coh1 with SAG0648 knocked out, Δ647-8, Coh1 with SAG0647 and SAG0648 knocked out; Δ80/pGBS80, Coh1 with GBS 80 knocked out but complemented with a high copy number plasmid expressing GBS 80. Asterisks identify the monomer of GBS 80 and GBS 104.)

The smear of immunoreactive material observed in the wild type strain, along with its disappearance in Δ80 and Δ104 mutants, is consistent with the notion that such high molecular weight structures are composed of covalently linked (SDS-resistant) GBS 80 and GBS 104 subunits. The immunoblotting with both anti-GBS 80 (α-GBS 80) and anti-GBS 104 (α-GBS 104) revealed that deletion of sortase SAG0648 also interferes with the assembly of high molecular weight species, whereas the knock out mutant of the second sortase (SAG0647), even if somehow reduced, still maintains the ability to form polymeric structures.

Total extracts form GBS were prepared as follows. Bacteria were grown in 50 ml of Todd-Hewitt broth (Difco) to an OD_{600nm} of 0.5-0.6 and successively pelleted. After two washes in PBS the pellet was resuspended and incubated 3 hours at 37°C with mutanolisin. Cells were then lysed with at

least three freezing-thawing cycles in dry ice and a 37°C bath. The lysate was then centrifuged to eliminate the cellular debris and the supernatant was quantified. Approximately 40 μg of each protein extract was separated on SDS-PAGE. The gel was then subjected to immunoblotting with mice antisera and detected with chemiluminescence.

Example 8: GBS 80 is polymerized by an AI-2 sortase

This example illustrates that GBS 80 can be polymerized not only by AI-1 sortases, but also by AI-2 sortases. Figure 42 shows total cell extract immunoblots of GBS 515 strain, which lacks AI-1. The left panel, where an anti-GBS 67 sera was used, shows that GBS 67 from AI-2 is assembled into high-molecular weight-complexes, suggesting the formation of a second type of pilus. The same high molecular structure is observed when GBS 80 is highly expressed by reintroducing the gene within a plasmid (pGBS 80). By using anti-GBS 80 (right panel) sera on the same extracts, again it is observed that, with GBS 80 over expression (515/pGBS 80), a high-molecular weight structure is assembled. This implies that, in the absence of AI-1 sortases, AI-2 sortases (SAG1405 and SAG1406) can complement the lacking function, still being able to assemble GBS 80 in a pilus structure.

Example 9: Coh1 produces a high molecular weight molecule, the GBS 80 pilin

This example illustrates that Coh1 produces a high molecular weight molecule, greater than 1000 kDa, which is the GBS 80 pilin. Figure 43 provides silver-stained electrophoretic gels that show that Coh1 produces two macromolecules. One of these macromolecules disappears in the Coh1 GBS 80 knock out cells, but does not disappear in the Coh1 GBS 52 knock out mutant cells. The last two lanes on the right were loaded with 15 times the amount loaded in the other lanes. This was done in order to be able to count the bands. By doing this, a conservative size estimate of the top bands was calculated by starting at 240 kDa and considering each of 14 higher bands as the result of consecutive additions of a GBS 80 monomer.

Coh1, wild type Coh1; Δ80, Coh1 cells with GBS 80 knocked out; Δ52, Coh1 cells with GBS 52 knocked out; Δ80/pGBS 80, Coh1 cells with GBS 80 knocked out and complemented with a high copy number construct expressing GBS 80.

Example 10. GBS 52 is a minor component of the GBS pilus

This example illustrates that GBS 52 is present in the GBS pilus and is a minor component of the pilus. Figure 45 shows an immunoblot of total cell extracts from a GBS Coh1 strain and a GBS Coh1 strain knocked out for GBS 52 (Δ52). The total cell extracts were immunoblotted anti-GBS 80 antisera (left) and anti-GBS 52 antisera (right). Immunoblotting was performed using a 3-8% Tris-acetate polyacrylamide gel (Invitrogen) which provided excellent separation of large molecular weight proteins (see figure 41). When the gel was incubated with anti-GBS 80 sera, the bands from the Coh1 wild-type strain appeared shifted when compared to the Δ52 mutant. This observation

indicated a different size of the pilus polymeric components in the two strains. When the same gel was stripped and incubated with anti-GBS 52 sera the high-molecular subunits in the Coh1 wild-type strain showed similar molecular size of those in the correspondent lane in the left panel. These findings confirmed that GBS 52 is indeed associated with GBS 80 macro-molecular structures but represents a minor component of the GBS pilus.

Example 11: Pilus structures are present in the supernatant of GBS bacterial cultures

This example illustrates that the pilus structure assembled in Coh1 GBS is present in the supernatant of a bacterial cell culture. Figure 46 shows an immunoblot where the protein extract of the supernatant from cultures of different GBS mutant strains (117 = Coh1 GBS 80 knockout; 159= Coh1 GBS 104 knockout; 202= Coh1 GBS 52 knockout; 206= Coh1 GBS sag0647 knockout; 208= Coh1 GBS sag0648 knockout; 197= Coh1 GBS sag0647/sag0648 knockout; 179= Coh1 GBS 80 knockout complemented with a high copy plasmid expressing GBS 80). GBS 80 antisera detects the presence of pilus structures in the appropriate Coh1 strains.

The protein extract was prepared as follows. Bacteria were grown in THB to an OD_{600nm} of 0.5-0.6 and the supernatant was separated from the cells by centrifugation. The supernatant was then filtered (∅ 0.2 μm) and 1 ml was added with 60% TCA for protein precipitation.
GBS pili were also extracted from the fraction of surface-exposed proteins in Coh1 strain and its GBS 80 knock out mutant as described hereafter. Bacteria were grown to an OD_{600nm} of 0.6 in 50 ml of THB at 37°C. Cells were washed once with PBS and the pellet was then resuspended in 0.1 M KPO4 pH 6.2, 40% sucrose, 10 mM MgCl2, 400U/ml mutanolysin and incubated 3 hours at 37°C. Protoplasts were separated by centrifugation and the supernatant was recovered and its protein content measured.

In order to study the dynamics of pilus production during different growth phases, 1 ml supernatant of a culture at different OD_{600nm} was TCA precipitated and loaded onto a 3-8% SDS-PAGE as described before. Figure 47 shows the corresponding Western blot with GBS 80 anti-sera. The first group of lanes (left five sample lanes) refer to a Coh1 strain growth (OD_{600nm} are noted above the lanes) whereas the second group of lanes (right five samples) are from a GBS 80 knock out strain over expressing GBS 80. The experiment shows that pilus macromolecular structures can be found in the supernatant in all of the growth phases tested.

Example 12: In GBS strain Coh1, only GBS 80 and a sortase (sag0647 or sag0648) is required for polymerization

This example describes requirements for pilus formation in Coh1. Figure 48 shows a Western blot of total protein extracts (prepared as described before) using anti-GBS 80 sera on Coh1 clones. (Coh1, wild type Coh1; Δ104, Coh1 knocked out for GBS 104, Δ647, Coh1 knocked out for sag0647, Δ648, Coh1 knocked for sag0648, Δ647-8, Coh1 knocked out for sag0647 and sag0648; 515, wild

type bacterial strain 515, which lacks an AI-1; p80 a high copy number plasmid which expresses GBS 80.) The data show that only the double sortase mutant is unable to polymerize GBS 80 indicating that the '*conditio sine qua non*' for pilus polymerization is the co-existence of GBS 80 with at least one sortase. This result leads to a reasonable assumption that SAG1405 and SAG1406 are responsible for polymerization in this strain.

Example 13: GBS 80 can be expressed in *L. lactis* under its own promoter and terminator sequences

This example demonstrates that *L. lactis*, a non-pathogenic bacterium, can express GBS AI polypeptides such as GBS 80. *L. lactis* M1363 (*J. Bacteriol. 154* (1983):1-9) was transformed with a construct encoding GBS 80. Briefly, the construct was prepared by cloning a DNA fragment containing the gene coding for GBS 80 under its own promoter and terminator sequences into plasmid pAM401 (a shuttle vector for *E. coli* and other Gram positive bacteria; *J. Bacteriol. 163* (1986):831-836). Total extracts of the transformed bacteria in log phase were separated on SDS-PAGE, transferred to membranes, and incubated with antiserum against GBS 80. A polypeptide corresponding to the molecular weight of GBS 80 was detected in the lanes containing total extracts of *L. lactis* transformed with the GBS 80 construct. See Figures 133A and 133B, lanes 6 and 7. This same polypeptide was not detected in the lane containing total extracts of *L. lactis* not transformed with the GBS 80 construct, lane 9. This example shows that *L. lactis* can express GBS 80 under its own promoter and terminator.

Example 14: *L. lactis* modified to express GBS AI-1 under the GBS 80 promoter and terminator sequences expresses GBS 80 in polymeric structures

This example demonstrates the ability of *L. lactis* to express GBS AI-1 polypeptides and to incorporate at least some of the polypeptides into oligomers. *L. lactis* was transformed with a construct containing the genes encoding GBS AI-1 polypeptides. Briefly, the construct was prepared by cloning a DNA fragment containing the genes for GBS 80, GBS 52, SAG0647, SAG0648, and GBS 104 under the GBS 80 promoter and terminator sequences into construct pAM401. The construct was transformed into *L. lactis* M1363. Total extracts of log phase transformed bacteria were separated on reducing SDS-PAGE, transferred to membranes, and incubated with antiserum against GBS 80. A polypeptide with a molecular weight corresponding to the molecular weight of GBS 80 was detected in the lanes containing *L. lactis* transformed with the GBS AI-1 encoding construct. See Figure 134, lane 2. In addition, the same lane also showed immunoreactivity of polypeptides having higher molecular weights than the polypeptide having the molecular weight of GBS 80. These higher molecular weight polypeptides are likely oligomers of GBS 80. Oligomers of similar molecular

weights were also observed on a Western blot of the culture supernatant of the transformed *L. lactis*. See lane 4 of Figure 135. Thus, this example shows that *L. lactis* transformed to express GBS AI-1 can efficiently polymerize GBS 80 in the form of a pilus. This pilus structure can likely be purified from either the cell culture supernatant or cell extracts.

Example 15: Cloning and Expression of *S. pneumoniae* Sp0462

This example describes the production of a clone encoding a Sp0462 polypeptide and expression of the clone. To produce a clone encoding Sp0462, the open reading frame encoding Sp0462 was amplified using primers that annealed within the full-length Sp0462 open reading frame sequence. Figure 150A provides a 893 amino acid sequence of Sp0462. The primers used to produce a clone encoding the Sp0462 polypeptide are shown in Figure 150B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 150A. Amplification of the open reading frame encoding Sp0462 using these primers produced the amplicon shown at lane 2 of the agarose gel provided in Figure 160. The Sp0462 clone encodes amino acid residues 38-862 of the 893 amino acid residue Sp0462 protein; the italicized residues in Figure 150A were eliminated. Figure 151A provides a schematic depiction of the recombinant Sp0462 polypeptide. Figure 151B shows a schematic depiction of the full-length Sp0462 polypeptide. Both the recombinant Sp0462 encoded by the clone and the full-length Sp0462 protein have two collagen binding protein type B (Cna B) domains and a von Hillebrand factor A (vWA) domain. The cloned recombinant Sp0462 lacks the LPXTG motif present in the full-length Sp0462 protein. Western blot analysis for expression of the Sp0462 clone did not result in detection of polypeptides with serum obtained from *S. pneumoniae*–infected patients (Figure 152A) or GBS 80 antiserum (Figure 152B).

Example 16: Cloning and Expression of *S. pneumoniae* Sp0463

This example describes the production of a clone encoding a Sp0463 polypeptide and detection of recombinant Sp0463 polypeptide expressed from the clone. To produce a clone encoding Sp0463, the open reading frame encoding Sp0463 was amplified using primers that annealed within the full-length Sp0463 open reading frame sequence. Figure 153A provides a 665 amino acid sequence of Sp0463. The primers used to produce the clone encoding Sp0463 polypeptide are shown in Figure 153B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 153A. Amplification of the open reading frame encoding Sp0463 using these primers produced the amplicon shown at lane 3 of the agarose gel provided in Figure 160. The Sp0463 clone encodes amino acid residues 23-627 of the 665 amino acid residue Sp0463 protein; the italicized residues in Figure 153A were eliminated. Figure 154A provides a schematic depiction of the recombinant Sp0463 polypeptide. Figure 154B shows a schematic depiction of the full-length Sp0463 polypeptide. Both the recombinant Sp0463 encoded by the clone and the full-length Sp0463 protein have a Cna B domain and an E box motif. The cloned recombinant

Sp0463 lacks the LPXTG motif present in the full-length Sp0463 protein. Expression of the Sp0463 clone resulted in the detection of a 60 kD polypeptide, the expected molecular weight of the recombinant Sp0463 polypeptide, by Western blot analysis. See Figure 155.

Example 17: Cloning and Expression of *S. pneumoniae* Sp0464

This example describes the production of a clone encoding a Sp0464 polypeptide and detection of recombinant Sp0464 polypeptide expressed from the clone. To produce a clone encoding Sp0464, the open reading frame encoding Sp0464 was amplified using primers that annealed either within the full-length Sp0464 open reading frame sequence. Figure 157A provides a 393 amino acid sequence of Sp0464. The primers used to produce a clone encoding the Sp0464 polypeptide are shown in Figure 157B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 157A. Amplification of the open reading frame encoding Sp0464 using these primers produced the amplicon shown at lane 4 of the agarose gel provided in Figure 160. The Sp0464 clone encodes amino acid residues 19-356 of the 393 amino acid residue Sp0464 protein; the italicized residues in Figure 157A were eliminated. Figure 158A provides a schematic depiction of the recombinant Sp0464 polypeptide. Figure 158B shows a schematic depiction of the full-length Sp0464 polypeptide. Both the recombinant Sp0464 encoded by the clone and the full-length Sp0464 protein have two Cna B domains. The cloned recombinant Sp0464 lacks the LPXTG motif present in the full-length Sp0464 protein. Expression of the Sp0464 clone resulted in the detection of a 38 kD polypeptide, the expected molecular weight of the recombinant Sp0464 polypeptide, by Western blot analysis. See Figure 159.

Example 18: Intranasal Immunization of Mice with Recombinant *L. lactis* Expressing GBS 80 and Subsequent Challenge

This example describes a method of intranasally immunizing mice using *L. lactis* that express GBS 80. Intranasal immunization consisted of 3 doses at days 0, 14 and 28, each dose administered in three consecutive days. Each day, groups of 3 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were immunized intranasally with 10^9 or 10^{10} CFU of the recombinant *Lactococcus lactis* suspended in 20 µl of PBS. In each immunization scheme negative (wild-type *L. lactis*) and positive (recombinant GBS80) control groups were used. The immune response of the dams was monitored by using serum samples taken on day 0 and 49. The female mice were bred 2-7 days after the last immunization (at approximately t= 36 – 37), and typically had a gestation period of 21 days. Within 48 hours of birth, the pups were challenged via I.P. with GBS in a dose approximately equal to an amount which would be sufficient to kill 90 % of immunized pups (as determined by empirical data gathered from PBS control groups). The GBS challenge dose is preferably administered in 50ml of THB medium. Preferably, the pup challenge takes place at 56 to 61 days after the first immunization. The challenge inocula were prepared starting from frozen

cultures diluted to the appropriate concentration with THB prior to use. Survival of pups was monitored for 5 days after challenge.

Example 19: Subcutaneous Immunization of Mice with Recombinant *L. lactis* Expressing GBS 80 and Subsequent Challenge

This example describes a method of subcutaneous immunization mice using *L. lactis* that express GBS 80. Subcutaneous immunization consists of 3 doses at days 0, 14 and 28. Groups of 3 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were injected subcutaneously with 10^9 or 10^{10} CFU of the recombinant *Lactococcus lactis* suspended in 100 µl of PBS. In each immunization scheme, negative (wild-type *L. lactis*) and positive (recombinant GBS80) control groups were used. The immune response of the dams was monitored by using serum samples taken on day 0 and 49. The female mice were bred 2-7 days after the last immunization (at approximately t= 36 – 37), and typically had a gestation period of 21 days. Within 48 hours of birth, the pups were challenged via I.P. with GBS in a dose approximately equal to an amount which would be sufficient to kill 90 % of immunized pups (as determined by empirical data gathered from PBS control groups). The GBS challenge dose is preferably administered in 50ml of THB medium. Preferably, the pup challenge takes place at 56 to 61 days after the first immunization. The challenge inocula were prepared starting from frozen cultures diluted to the appropriate concentration with THB prior to use. Survival of pups was monitored for 5 days after challenge.

Example 20: Immunization of Mice with GAS AI polypeptides and Subsequent Intranasal Challenge

This example describes a method of immunizing mice with GAS AI polypeptides and subsequently intranasally challenging the mice with GAS bacteria. Groups of 10 CD1 female mice aged between 6 and 7 weeks are immunized with a combination of GAS antigens of the invention GAS 15, GAS 16, and GAS 18, (15 µg of each recombinant antigen, derived from M1 strain SF370) or *L. lactis* expressing the M1 strain SF370 adhesin island, suspended in 100 µl of suitable solution. Each group receives 3 doses at days 0, 21 and 45. Immunization is performed through subcutaneous or intraperitoneal injection for the GAS 15, GAS 16, GAS 18 protein combination. The protein combination is administered with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. Immunization is performed intranasally for the *L. lactis* expressing the M1 strain SF370 adhesin island. In each immunization scheme negative and positive control groups are used.

The negative control group for the mice immunized with the GAS 15, GAS 16, GAS 18 protein combination included mice immunized with PBS. The negative control group for the mice immunized with *L. lactis* expressing the M1 strain SF370 adhesin island, included mice immunized

with either wildtype *L. lactis* or *L. lactis* transformed with the pAM401 expression vector lacking any cloned adhesin island sequence.

The positive control groups included mice immunized with purified M1 strain SF370 M protein.

Immunized mice are then anaesthetized with Zoletil and challenged intranasally with a 25 μL suspension containing 1.2×10^6 or 1.2×10^8 CFU of ISS 3348 in THB. Animals are observed daily and checked for survival.

Example 21: Active Maternal Immunization Assay

As used herein, an Active Maternal Immunization assay refers to an *in vivo* protection assay where female mice are immunized with the test antigen composition. The female mice are then bred and their pups are challenged with a lethal dose of GBS. Serum titers of the female mice during the immunization schedule are measured as well as the survival time of the pups after challenge.

Mouse immunization

Specifically, groups of 4 CD-1 outbred female mice 6-8 weeks old (Charles River Laboratories, Calco Italy) are immunized with one or more GBS antigens, (20 μg of each recombinant GBS antigen), suspended in 100 μl of PBS. Each group receives 3 doses at days 0, 21 and 35. Immunization is performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. In each immunization scheme negative and positive control groups are used.

Immune response is monitored by using serum samples taken on day 0 and 49. The sera are analyzed as pools from each group of mice.

Active maternal immunization

A maternal immunization/neonatal pup challenge model of GBS infection was used to verify the protective efficacy of the antigens in mice. The mouse protection study was adapted from Rodewald et al. (Rodewald et al. J. Infect. Diseases 166, 635 (1992)). In brief, CD-1 female mice (6-8 weeks old) were immunized before breeding, as described above. The mice received 20 μg of protein per dose when immunized with a single antigen and 60 μg of protein per dose (15 μg of each antigen) when immunized with the combination of antigens. Mice were bred 2-7 days after the last immunization. Within 48 h of birth, pups were injected intraperitoneally with 50 μl of GBS culture. Challenge inocula were prepared starting from frozen cultures diluted to the appropriate concentration with THB before use. In preliminary experiments (not shown), the challenge doses per pup for each strain tested were determined to cause 90% lethality. Survival of pups was monitored for 2 days after challenge. Protection was calculated as (percentage

deadControl minus percentage deadVaccine) divided by percentage deadControl multiplied by 100. Data were evaluated for statistical significance by Fisher's exact test.

Embodiments of the Invention

The invention encompasses, but is not limited to, the embodiments enumerated below.

1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.

2. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.

3. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.

1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.

2. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.

3. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.

4. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide comprises a sortase substrate motif.

5. The immunogenic composition of embodiment 4 wherein the sortase substrate motif is an LPXTG motif.

6. The immunogenic composition of embodiment 5 wherein the LPXTG motif is represented by the amino acid sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.

7. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.

8. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.

9. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.

10. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide is capable of associating with an epithelial cell surface.

11. The immunogenic composition of embodiment 10 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

12. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide is a full-length GBS AI protein.

13. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide is a fragment of a full-length GBS AI protein.

14. The immunogenic composition of embodiment 13 wherein the fragment comprises at least 7 contiguous amino acid residues of the GBS AI protein.

15. The immunogenic composition of embodiment 2 wherein the GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

16. The immunogenic composition of embodiment 3 wherein the GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

17. The immunogenic composition of embodiment 15 wherein the GBS AI polypeptide is GBS 80.

18. The immunogenic composition of any of embodiments 1-3 or 15-17 wherein the oligomeric form is a hyperoligomer.

19. The immunogenic composition of any of embodiments 1-3, or 15-17 further comprising a Gram positive bacterium antigen not associated with an AI.

20. The immunogenic composition of embodiment 19 wherein the antigen is selected from the group consisting of GBS 322 and GBS 276.

21. The immunogenic composition of embodiment 20 wherein the antigen is GBS 322.

22. An immunogenic composition comprising a purified Gram positive bacteria adhesin island (AI) polypeptide in an oligomeric form.

23. The immunogenic composition of embodiment 22 wherein the Gram positive bacteria is of a genus selected from the group consisting of *Streptococcus*, *Enterococcus*, *Staphylococcus*, or *Listeria*.

24. The immunogenic composition of embodiment 23 wherein the Gram positive bacteria is of the genus *Streptococcus*.

25. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide comprises a sortase substrate motif.

26. The immunogenic composition of embodiment 25 wherein the sortase substrate motif is an LPXTG motif.

27. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to adhere to epithelial cells.

28. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to invade epithelial cells.

29. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to translocate through an epithelial cell layer.

30. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is capable of associating with an epithelial cell surface.

31. The immunogenic composition of embodiment 30 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

32. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is a full-length Gram positive bacteria AI protein.

33. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is a fragment of a full-length Gram positive bacteria AI protein.

34. The immunogenic composition of embodiment 33 wherein the fragment comprises at least 7 contiguous amino acid residues of the Gram positive bacteria AI protein.

35. The immunogenic composition of embodiment 24 wherein the genus *Streptococcus* bacteria is Group A Streptococcus (GAS) bacteria and the Gram positive bacteria AI polypeptide is a GAS AI polypeptide.

36. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-1.

37. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-2.

38. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-3.

39. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-4.

40. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide comprises a sortase substrate motif.

41. The immunogenic composition of embodiment 40 wherein the sortase substrate motif is an LPXTG motif.

42. The immunogenic composition of embodiment 41 wherein the LPXTG motif is represented by XXXXG, wherein the X at the first amino acid position is an L, a V, an E, or a Q, wherein the X at the second amino acid position is P if the X at the first amino acid position is an L, the X at the second amino acid position is a V if the X at the first amino acid position is an E or a Q, or the X at the second amino acid position is a V or a P if the X at the first amino acid position is a V, wherein the X at the third amino acid position is any amino acid residue, and wherein the X at the fourth amino acid position is a T if the X at the first amino acid position is a V, an E, or a Q, or the X at the fourth amino acid position is a T, an S, or an A if the X at the first amino acid position is an L.

43. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to adhere to epithelial cells.

44. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to invade epithelial cells.

45. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to translocate through an epithelial cell layer.

46. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide is capable of associating with an epithelial cell surface.

47. The immunogenic composition of embodiment 46 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

48. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide is a full-length GAS AI protein.

49. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide is a fragment of a full-length GAS AI protein.

50. The immunogenic composition of embodiment 49 wherein the fragment comprises at least 7 contiguous amino acid residues of the GAS AI protein.

51. The immunogenic composition of embodiment 36 wherein the GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650_fimbrial, DSM2071_fimbrial, and fragments thereof.

52. The immunogenic composition of embodiment 37 wherein the GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.

53. The immunogenic composition of embodiment 38 wherein the GAS AI-3 polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040_fimbrial, ISS3776_fimbrial, ISS4959_fimbrial, and fragments thereof.

53. The immunogenic composition of embodiment 39 wherein the GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538_fimbrial, and fragments thereof.

54. The immunogenic composition of embodiment 24 wherein the *Streptococcus* bacteria is *Streptococcus pneumoniae* and the Gram positive bacteria AI polypeptide is a *S. pneumoniae* AI polypeptide.

55. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide comprises a sortase substrate motif.

56. The immunogenic composition of embodiment 55 wherein the sortase substrate motif is an LPXTG motif.

57. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to adhere to epithelial cells.

58. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to invade epithelial cells.

59. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to translocate through an epithelial cell layer.

60. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is capable of associating with an epithelial cell surface.

61. The immunogenic composition of embodiment 60 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

62. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is a full-length *S. pneumoniae* AI protein.

63. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is a fragment of a full-length *S. pneumoniae* AI protein.

64. The immunogenic composition of embodiment 63 wherein the fragment comprises at least 7 contiguous amino acid residues of the *S. pneumoniae* AI protein.

65. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is selected from the group consisting of SP0462, SP0463, SP0464, orf3_670, orf4_670, orf5_670, ORF3_14CSR, ORF4_14CSR, ORF5_14CSR, ORF3_19AH, ORF4_19AH, ORF5_19AH, ORF3_19FTW, ORF4_19FTW, ORF5_19FTW, ORF3_23FP, ORF4_23FP, ORF5_23FP, ORF3_23FTW, ORF4_23FTW, ORF5_23FTW, ORF3_6BF, ORF4_6BF, ORF5_6BF, ORF3_6BSP, ORF4_6BSP, ORF5_6BSP, ORF3_9VSP, ORF4_9VSP, ORF5_9VSP, and fragments thereof.

66. The immunogenic composition of any one of embodiments 22-24, 35-39, 51-54, or 65 wherein the oligomeric form is a hyperoligomer.

67. The immunogenic composition of any one of embodiments 22-24, 35-39, 51-54, or 65 further comprising a Gram positive bacteria antigen not associated with an AI.

68. The immunogenic composition of embodiment 67 wherein the antigen is selected from the group consisting of GBS 322 and GBS 276.

69. An immunogenic composition comprising a first and a second Group B Streptococcus (GBS) adhesin island (AI) polypeptide.

70. The immunogenic composition of embodiment 69 wherein a full-length polynucleotide sequence encoding for the first GBS AI polypeptide is not present in a GBS bacteria genome comprising a polynucleotide sequence encoding for the second GBS AI polypeptide.

71. The immunogenic composition of embodiment 69 wherein polynucleotides encoding the first and the second GBS AI polypeptide are each present in genomes of more than one GBS serotype and strain isolate.

72. The immunogenic composition of embodiment 69 wherein the first GBS AI polypeptide is encoded by a GBS AI-1.

73. The immunogenic composition of embodiment 69 wherein the first GBS AI polypeptide is encoded by a GBS AI-2.

74. The immunogenic composition of embodiment 72 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.

75. The immunogenic composition of embodiment 73 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.

76. The immunogenic composition of embodiment 72 wherein the second GBS AI polypeptide is encoded by a GBS AI-1.

77. The immunogenic composition of embodiment 73 wherein the second GBS AI polypeptide is encoded by a GBS AI-1.

78. The immunogenic composition of embodiment 72 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

79. The immunogenic composition of embodiment 73 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

80. The immunogenic composition of embodiment 74 or 75 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.

81. The immunogenic composition of embodiment 76 or 77 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.

82. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide comprises a sortase substrate motif.

83. The immunogenic composition of embodiment 82 wherein the sortase substrate motif is an LPXTG motif.

84. The immunogenic composition of embodiment 83 wherein the LPXTG motif is represented by the sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.

85. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.

86. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.

87. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.

88. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide is capable of associating with an epithelial cell surface.

89. The immunogenic composition of embodiment 88 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

90. The immunogenic composition of any of embodiments 69-77 wherein the first GBS AI polypeptide is a full-length GBS AI protein.

91. The immunogenic composition of any of embodiments 69-77 wherein the first GBS AI polypeptide is a fragment of a full-length GBS AI protein.

92. The immunogenic composition of embodiment 91 wherein the fragment comprises at least 7 contiguous amino acid residues of the first GBS AI protein.

93. The immunogenic composition of any one of embodiments 69-79 wherein the first GBS AI polypeptide is in oligomeric form.

94. The immunogenic composition of any one of embodiments 69-77 wherein the second GBS AI polypeptide is in oligomeric form.

95. The immunogenic composition of any one of embodiments 69-79 wherein the first and the second GBS AI polypeptide are associated in a single oligomeric form.

96. The immunogenic composition of embodiment 95 wherein the first and the second GBS AI polypeptides are chemically associated.

97. The immunogenic composition of embodiment 95 wherein the first and the second GBS AI polypeptides are physically associated.

98. The immunogenic composition of embodiment 93 wherein the oligomeric form is a hyperoligomer.

99. The immunogenic composition of embodiment 94 wherein the oligomeric form is a hyperoligomer.

100. The immunogenic composition of embodiment 76 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 104.

101. The immunogenic composition of embodiment 74 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 67.

102. The immunogenic composition of any one of embodiments 69-79, 100, or 101 further comprising a GBS polypeptide not associated with an AI.

103. The immunogenic composition of embodiment 102 wherein the GBS polypeptide not associated with an AI is selected from the group consisting of GBS 322 and GBS 276.

104. The immunogenic composition of embodiment 103 wherein the GBS polypeptide not associated with an AI is GBS 322.

105. An immunogenic composition comprising a first and a second Gram positive bacteria adhesin island (AI) polypeptide.

106. The immunogenic composition of embodiment 105 wherein a full length polynucleotide sequence encoding for the first Gram positive bacteria AI polypeptide is not present in a genome of a Gram positive bacteria comprising a full length polynucleotide sequence encoding for the second Gram positive bacteria AI polypeptide.

107. The immunogenic composition of embodiment 105 wherein polynucleotides encoding the first and the second Gram positive bacteria AI polypeptide are each present in genomes of more than one Gram positive bacteria serotype and strain isolate.

108. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are of different Gram positive bacteria species.

109. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are of the same Gram positive bacteria species.

110. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are from different AI subtypes.

111. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are from the same AI subtype.

112. The immunogenic composition of embodiment 105 wherein the first Gram positive bacteria AI polypeptide has detectable surface exposure on a first Gram positive bacteria strain or serotype but not a second Gram positive bacteria strain or subtype and the second Gram positive bacteria AI polypeptide has detectable surface exposure on the second Gram positive bacteria strain or serotype but not the first Gram positive bacteria strain or serotype.

113. The immunogenic composition of embodiment 105 wherein the Gram positive bacteria is *S. pneumonaie*, *S. mutans*, *E. faecalis*, *E. faecium*, *C. difficile*, *L. monocytogenes*, or *C. diphtheriae*.

114. The immunogenic composition of any of embodiments 105-113 wherein the first and the second Gram positive bacteria AI polypeptides comprise a sortase substrate motif.

115. The immunogenic composition of embodiment 114 wherein the sortase substrate motif is an LPXTG motif.

116. The immunogenic composition of embodiment 115 wherein the LPXTG motif is represented by XXXXG, wherein the X at amino acid position 1 is an L, a V, an E, an I, an F, or a Q, wherein X at amino acid position 2 is a P if X at amino acid position 1 is an L, an I, or an F, wherein X at amino acid position 2 is a V if X at amino acid position 1 is a E or a Q, wherein X at amino acid position 2 is a V or a P if X at amino acid position 1 is a V, wherein X at amino acid position 3 is any amino acid residue, wherein X at amino acid position 4 is a T if X at amino acid position 1 is a V, E, I, F, or Q, and wherein X at amino acid position 4 is a T, S, or A if X at amino acid position 1 is an L.

117. The immunogenic composition of embodiment 105 wherein the first Gram positive bacteria AI polypeptide is a first Group A Streptococcus (GAS) AI polypeptide.

118. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide comprises a sortase substrate motif.

119. The immunogenic composition of embodiment 118 wherein the sortase substrate motif is an LPXTG motif.

120. The immunogenic composition of embodiment 119 wherein the LPXTG motif is represented by XXXXG, wherein the X at the first amino acid position is an L, a V, an E, or a Q, wherein the X at the second amino acid position is P if the X at the first amino acid position is an L, the X at the second amino acid position is a V if the X at the first amino acid position is an E or a Q, or the X at the second amino acid position is a V or a P if the X at the first amino acid position is a V, wherein the X at the third amino acid position is any amino acid residue, and wherein the X at the fourth amino acid position is a T if the X at the first amino acid position is a V, an E, or a Q, or the X at the fourth amino acid position is a T, an S, or an A if the X at the first amino acid position is an L.

121. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide affects the ability of GAS bacteria to adhere to epithelial cells.

122. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide affects the ability of GAS bacteria to invade epithelial cells.

123. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide affects the ability of GAS bacteria to translocate through an epithelial cell layer.

124. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is capable of associating with an epithelial cell surface.

125. The immunogenic composition of embodiment 117 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

126. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a full-length GAS AI protein.

127. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a fragment of a full-length GAS AI protein.

128. The immunogenic composition of embodiment 127 wherein the fragment comprises at least 7 contiguous amino acid residues of the GAS AI protein.

129. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-1 polypeptide.

130. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-2 polypeptide.

131. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-3 polypeptide.

132. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-4 polypeptide.

133. The immunogenic composition of any one of embodiments 117 or 129-132 wherein the second Gram positive bacteria AI polypeptide is a second GAS AI polypeptide.

134. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-1 polypeptide.

135. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-2 polypeptide.

136. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-3 polypeptide.

137. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-4 polypeptide.

138. The immunogenic composition of embodiment 129 wherein the first GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650_fimbrial, DSM2071_fimbrial, and fragments thereof.

139. The immunogenic composition of embodiment 130 wherein the first GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.

140. The immunogenic composition of embodiment 131 wherein the first GAS AI-3 polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040_fimbrial, ISS3776_fimbrial, ISS4959_fimbrial, and fragments thereof.

141. The immunogenic composition of embodiment 132 wherein the first GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538_fimbrial, and fragments thereof.

142. The immunogenic composition of embodiment 134 wherein the second GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650_fimbrial, DSM2071_fimbrial, and fragments thereof.

143. The immunogenic composition of embodiment 135 wherein the second GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.

144. The immunogenic composition of embodiment 136 wherein the second GAS AI-3 polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040_fimbrial, ISS3776_fimbrial, ISS4959_fimbrial, and fragments thereof.

145. The immunogenic composition of embodiment 137 wherein the second GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538_fimbrial, and fragments thereof.

146. The immunogenic composition of any one of embodiments 117-132 or 138-141 wherein the second Gram positive bacteria AI polypeptide is a Group B Streptococcus (GBS) AI polypeptide.

147. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide comprises a sortase substrate motif.

148. The immunogenic composition of embodiment 147 wherein the sortase substrate motif is an LPXTG motif.

149. The immunogenic composition of embodiment 148 wherein the LPXTG motif is represented by the amino acid sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.

150. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.

151. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.

152. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.

153. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is capable of associating with an epithelial cell surface.

154. The immunogenic composition of embodiment 146 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

155. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a full-length GBS AI protein.

156. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a fragment of a full-length GBS AI protein.

157. The immunogenic composition of embodiment 156 wherein the fragment comprises at least 7 contiguous amino acid residues of the GBS AI protein.

158. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a GBS AI-1 polypeptide.

159. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a GBS AI-2 polypeptide.

160. The immunogenic composition of embodiment 158 wherein the GBS AI-1 polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

161. The immunogenic composition of embodiment 159 wherein the GBS AI-2 polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

162. The immunogenic composition of any one of embodiments 117-132 or 138-141 wherein the second Gram positive bacteria AI polypeptide is a *Streptococcus pneumoniae* AI polypeptide.

163. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide comprises a sortase substrate motif.

164. The immunogenic composition of embodiment 163 wherein the sortase substrate motif is an LPXTG motif.

165. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to adhere to epithelial cells.

166. The immunogenic composition of embodiment 162 *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to invade epithelial cells.

167. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide affects the ability of *S. pneumoniae* to translocate through an epithelial cell layer.

168. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide is capable of associating with an epithelial cell surface.

169. The immunogenic composition of embodiment 168 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

170. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide is a full-length *S. pneumoniae* AI protein.

171. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide is a fragment of a full-length *S. pneumoniae* AI protein.

172. The immunogenic composition of embodiment 162 wherein the fragment comprises at least 7 contiguous amino acid residues of the *S. pneumoniae* AI protein.

173. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide is selected from the group consisting of SP0462, SP0463, SP0464, orf3_670, orf4_670, orf5_670, ORF3_14CSR, ORF4_14CSR, ORF5_14CSR, ORF3_19AH, ORF4_19AH, ORF5_19AH, ORF3_19FTW, ORF4_19FTW, ORF5_19FTW, ORF3_23FP, ORF4_23FP, ORF5_23FP, ORF3_23FTW, ORF4_23FTW, ORF5_23FTW, ORF3_6BF, ORF4_6BF, ORF5_6BF, ORF3_6BSP, ORF4_6BSP, ORF5_6BSP, ORF3_9VSP, ORF4_9VSP, ORF5_9VSP, and fragments thereof.

174. The immunogenic composition of any one of embodiments 105-117 wherein the first Gram positive bacteria AI polypeptide is in oligomeric form.

175. The immunogenic composition of embodiment 174 wherein the oligomeric form is a hyperoligomer.

176. The immunogenic composition of embodiment 174 wherein the second Gram positive bacteria AI polypeptide is in oligomeric form.

177. The immunogenic composition of embodiment 176 wherein the oligomeric form is a hyperoligomer.

178. The immunogenic composition of embodiment 176 wherein the first and the second Gram positive bacteria AI polypeptide are associated in a single oligomeric form.

179. The immunogenic composition of embodiment 178 wherein the first and the second Gram positive bacteria AI polypeptide are chemically associated.

180. The immunogenic composition of embodiment 178 wherein the first and the second Gram positive bacteria AI polypeptide are physically associated.

181. The immunogenic composition of any one of embodiments 105-117 further comprising a Gram positive bacteria polypeptide not associated with an AI.

182. The immunogenic composition of embodiment 181 wherein the Gram positive bacteria polypeptide not associated with an AI is selected from the group consisting of GBS 322 and GBS 276.

183. The immunogenic composition of embodiment 182 wherein the Gram positive bacteria polypeptide not associated with an AI is GBS 322.

184. A modified Gram positive bacterium adapted to produce increased levels of AI surface protein.

185. The modified Gram positive bacterium of embodiment 184 wherein the AI surface protein is in oligomeric form.

186. The modified Gram positive bacterium of embodiment 185 wherein the oligomeric form is a hyperoligomer.

187. The modified Gram positive bacterium of any one of embodiments 184-186 which is a Group B Streptococcus bacterium.

188. The modified Gram positive bacterium of any one of embodiments 184-186 which is a Group A Streptococcus bacterium.

189. The modified Gram positive bacterium of any one of embodiments 184-186 which is a non-pathogenic Gram positive bacterium.

190. The modified Gram positive bacterium of embodiment 189 wherein the non-pathogenic Gram positive bacterium is *Streptococus gordonii.*

191. The modified Gram positive bacterium of embodiment 189 wherein the non-pathogenic Gram positive bacterium is *Lactococcus lactis.*

192. The modified Gram positive bacterium of any one of embodiments 184-186 which has been inactivated and wherein the AI surface protein is exposed on the surface of the Gram positive bacterium.

193. The modified Gram positive bacterium of any one of embodiments 184-186 which has been attenuated and wherein the AI surface protein is exposed on the surface of the Gram positive bacterium.

194. The modified GBS bacterium of embodiment 187 which has been inactivated and wherein the AI surface protein is exposed on the surface of the GBS bacterium.

195. The modified GBS bacterium of embodiment 187 which has been attenuated and wherein the AI surface protein is exposed on the surface of the GBS bacterium.

196. The modified GAS bacterium of embodiment 188 which has been inactivated and wherein the AI surface protein is exposed on the surface of the GAS bacterium.

197. The modified GAS bacterium of embodiment 188 which has been attenuated and wherein the AI surface protein is exposed on the surface of the GAS bacterium.

198. The modified non-pathogenic bacterium of embodiment 189 which has been inactivated and wherein the AI surface protein is exposed on the surface of the non-pathogenic Gram positive bacterium.

199. The modified non-pathogenic bacterium of embodiment 189 which has been attenuated and wherein the AI surface protein is exposed on the surface of the non-pathogenic Gram positive bacterium.

200. A method for manufacturing an oligomeric adhesin island (AI) surface antigen comprising:

culturing a Gram positive bacterium that expresses an oligomeric AI surface antigen and

isolating the expressed oligomeric AI surface antigen.

201. The method of embodiment 200 wherein the step of isolating is performed by collecting said oligomeric AI surface antigen from Gram positive bacterium secretions in the Gram positive bacterium culture.

202. The method of embodiment 200 further comprising a step of purifying.

203. The method of embodiment 202 wherein the oligomeric AI surface antigen is purified from the Gram positive bacterium cell surface.

204. The method of embodiment 200 wherein the Gram positive bacterium is adapted for increased AI protein expression.

205. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is a Group A Streptococcus bacterium.

206. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is a Group B Streptococcus bacterium.

207. The method of any one of embodiments 200-204 wherein the oligomeric AI surface antigen is in hyperoligomeric form.

208. The method of embodiment 200 wherein the Gram positive bacterium expresses the oligomeric AI surface antigen recombinantly.

209. The method of embodiment 208 wherein the Gram positive bacterium further manipulated expresses at least 1 AI sortase.

210. The modified Gram positive bacterium of any one of embodiments 184-186 which is a *S. pneumoniae* bacterium.

211. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is *S. pneumoniae.*

WE CLAIM:

1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.

2. The immunogenic composition of claim 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.

3. The immunogenic composition of claim 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.

4. The immunogenic composition of claim 2 wherein the GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

5. The immunogenic composition of claim 3 wherein the GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

6. The immunogenic composition of claim 4 wherein the GBS AI polypeptide is GBS 80.

7. The immunogenic composition of any of claims 1-6 wherein the oligomeric form is a hyperoligomer.

8 (22). An immunogenic composition comprising a purified Gram positive bacteria adhesin island (AI) polypeptide in an oligomeric form.

9 (23). The immunogenic composition of claim 8 wherein the Gram positive bacteria is of a genus selected from the group consisting of *Streptococcus*, *Enterococcus*, *Staphylococcus*, *Clostridium*, *Corynebacterium*, or *Listeria*.

10 (24). The immunogenic composition of claim 9 wherein the Gram positive bacteria is of the genus *Streptococcus*.

11 (35). The immunogenic composition of claim 10 wherein the genus *Streptococcus* bacteria is Group A Streptococcus (GAS) bacteria and the Gram positive bacteria AI polypeptide is a GAS AI polypeptide.

12 (36). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-1.

13 (37). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-2.

14 (38). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-3.

15 (39). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-4.

16 (66). The immunogenic composition of any one of claims 8-15 wherein the oligomeric form is a hyperoligomer.

17. An immunogenic composition comprising a first and a second Group B Streptococcus (GBS) adhesin island (AI) polypeptide.

18. The immunogenic composition of claim 17 wherein the first GBS AI polypeptide is encoded by a GBS AI-1.

19. The immunogenic composition of claim 18 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.

20. The immunogenic composition of claim 18 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

21. The immunogenic composition of claim 19 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.

22. The immunogenic composition of claim 19 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 67.

23. An immunogenic composition comprising a first and a second Gram positive bacteria adhesin island (AI) polypeptide.

24. The immunogenic composition of claim 23 wherein the Gram positive bacteria is *Streptococcus*, *Enterococcus*, *Staphylococcus*, *Clostridium*, *Corynebacterium*, or *Listeria*.

25. The immunogenic composition of claim 23 wherein the first Gram positive bacteria AI polypeptide is a first Group A Streptococcus (GAS) AI polypeptide.

26. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-1 polypeptide.

27. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-2 polypeptide.

28. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-3 polypeptide.

29. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-4 polypeptide.

30. The immunogenic composition of any one of claims 25-29 wherein the second Gram positive bacteria AI polypeptide is a second GAS AI polypeptide.

31. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-1 polypeptide.

32. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-2 polypeptide.

33. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-3 polypeptide.

34. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-4 polypeptide.

35. A modified Gram positive bacterium adapted to produce increased levels of AI surface protein.

36. The modified Gram positive bacterium of claim 35 wherein the AI surface protein is in oligomeric form.

37. The modified Gram positive bacterium of claim 36 wherein the oligomeric form is a hyperoligomer.

38. The modified Gram positive bacterium of any one of claims 35-37 which is a non-pathogenic Gram positive bacterium.

39. The modified Gram positive bacterium of claim 38 wherein the non-pathogenic Gram positive bacterium is *Lactococcus lactis.*

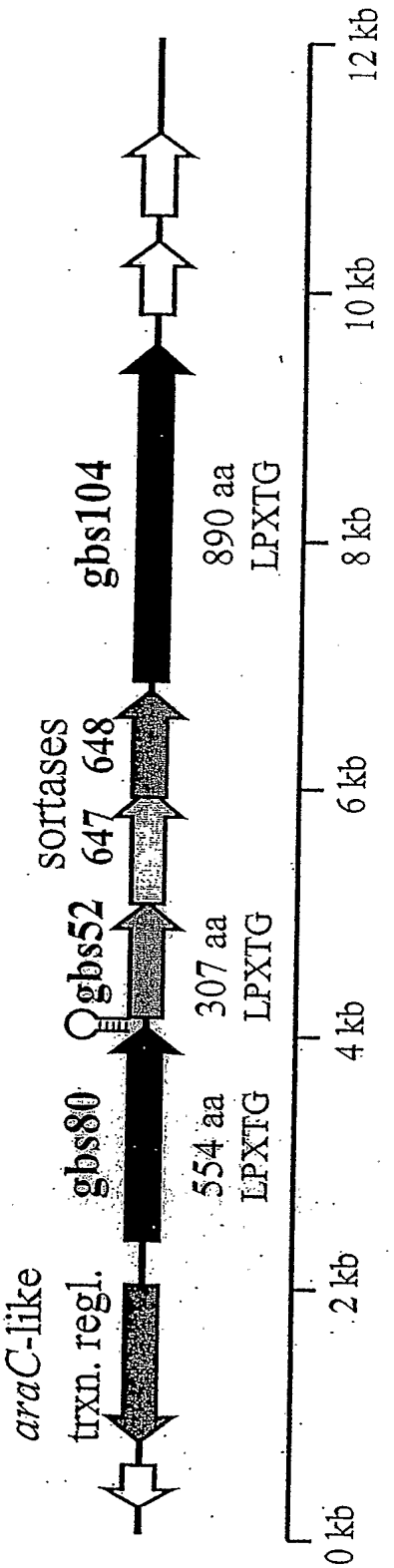
40. A method for manufacturing an oligomeric adhesin island (AI) surface antigen comprising:

culturing a Gram positive bacterium that expresses an oligomeric AI surface antigen and

isolating the expressed oligomeric AI surface antigen.

PCT/US2005/027239

FIGURE 1: Adhesion Island 1



PCT/US05/27239

Figure 2: Conservation of AI-1 in GBS serotypes and strain isolates

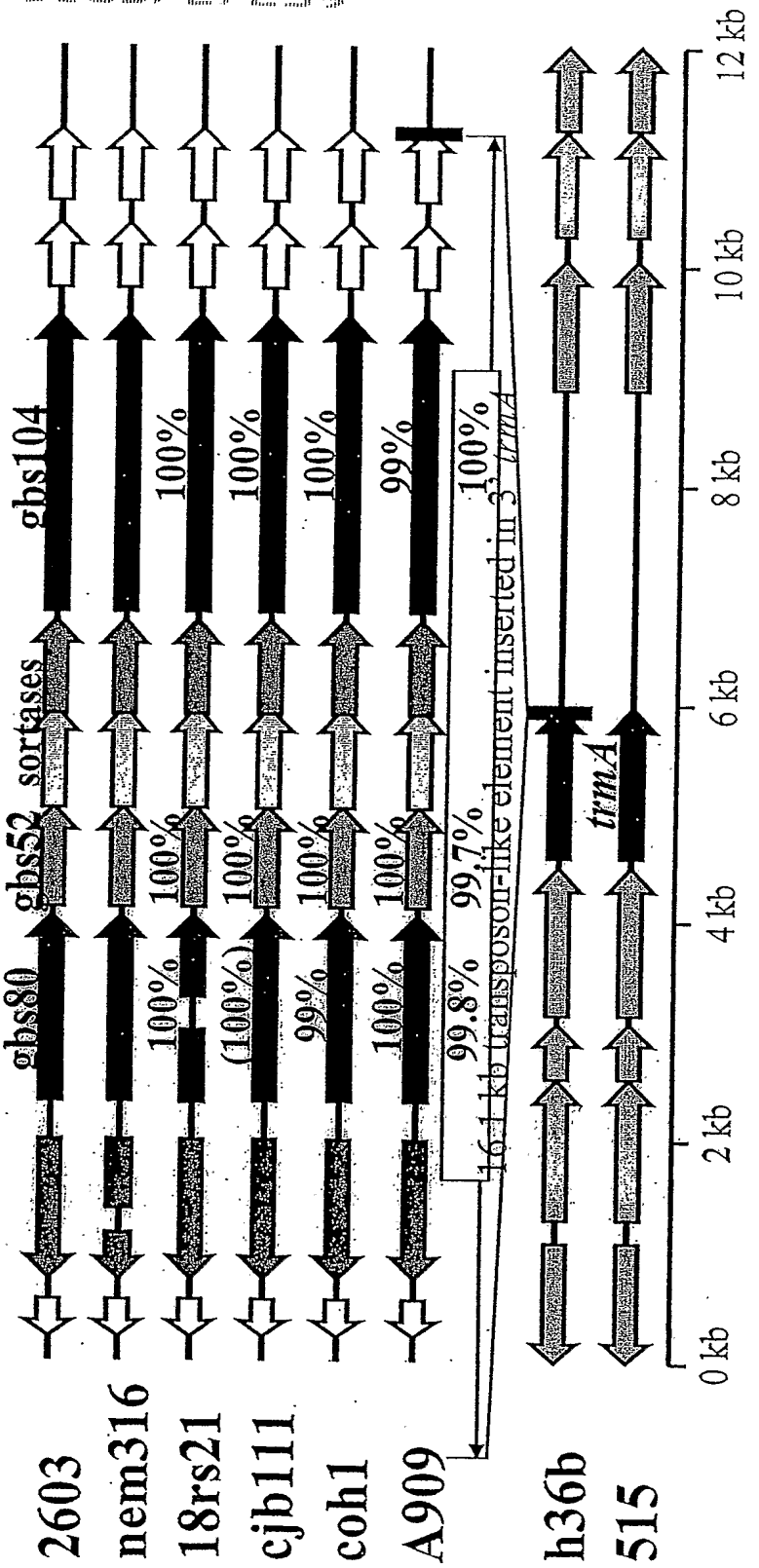


FIGURE 3: Correlation of AI-1 and AI-2 within GBS serotype V, strain isolate 2603 genome

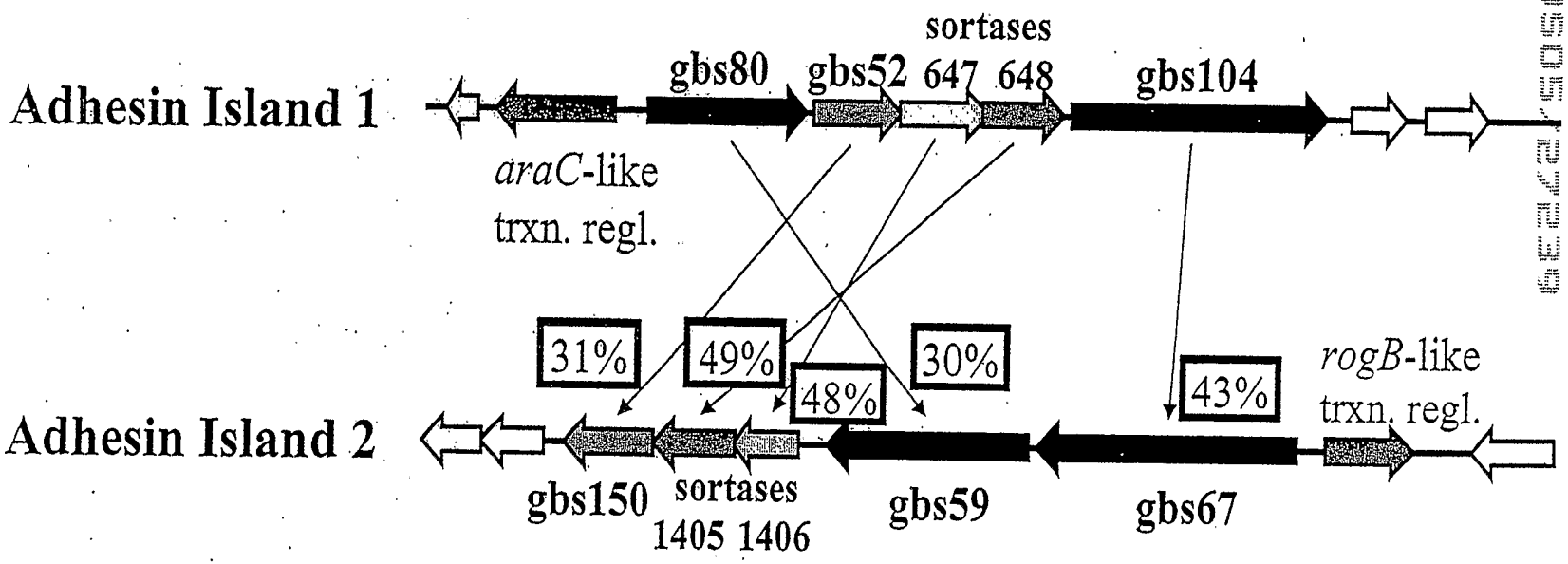


Figure 4: Identification and Variance of AI-2 in Several GBS Serotypes and Strain Isolates

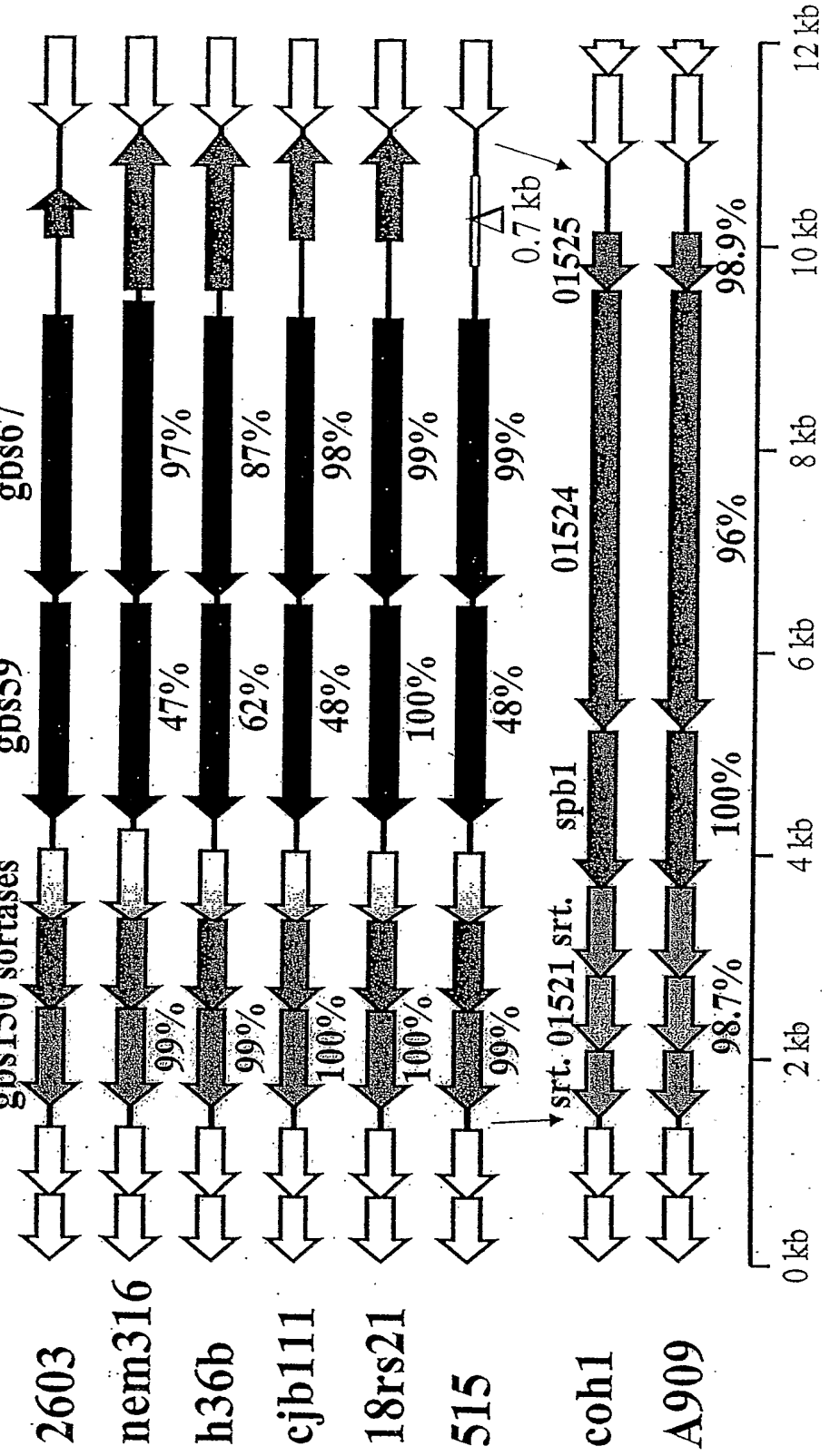


Figure 5: Purified gbs80 protein binds fibronectin and fibrinogen in an ELISA

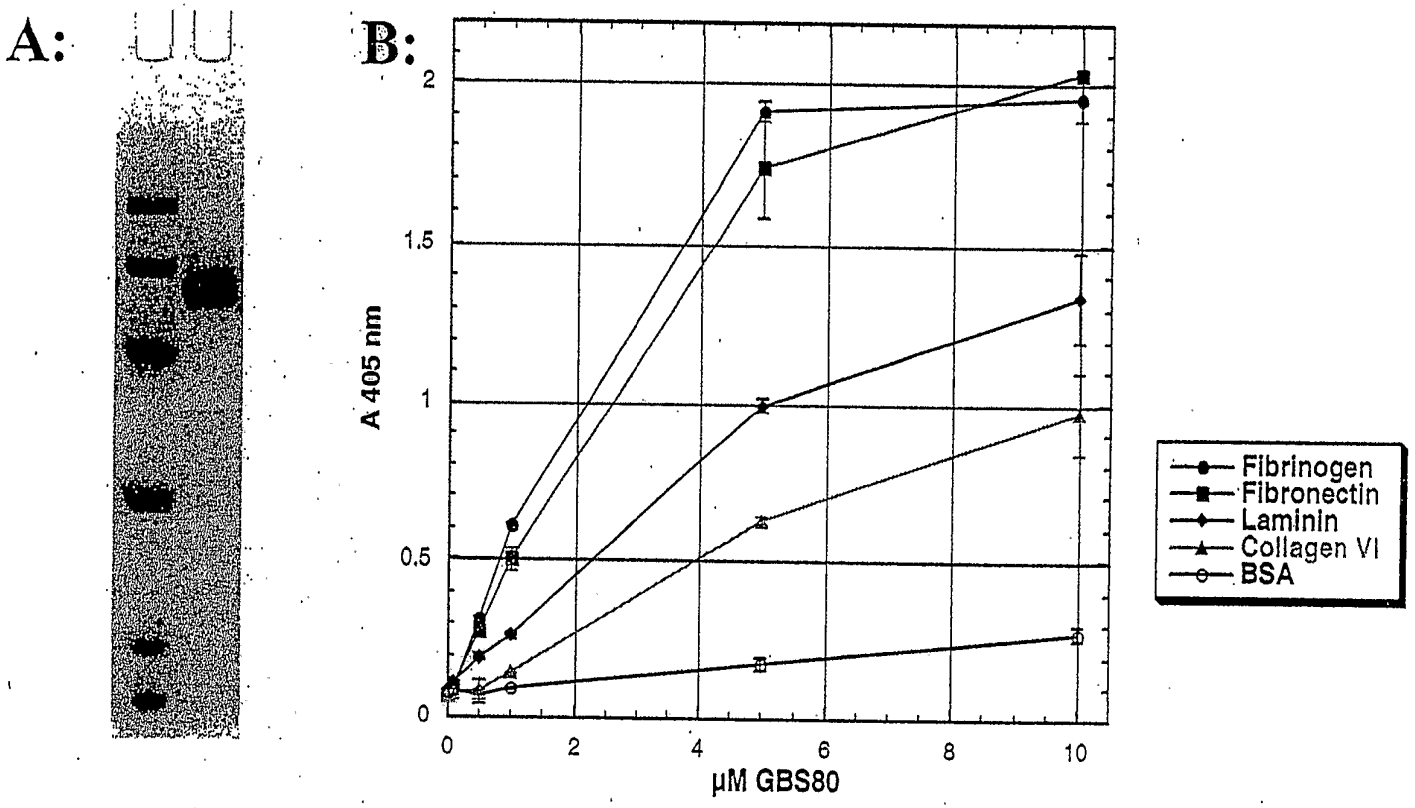


Figure 6: Adhesion Island I is an operon by RT-PCR

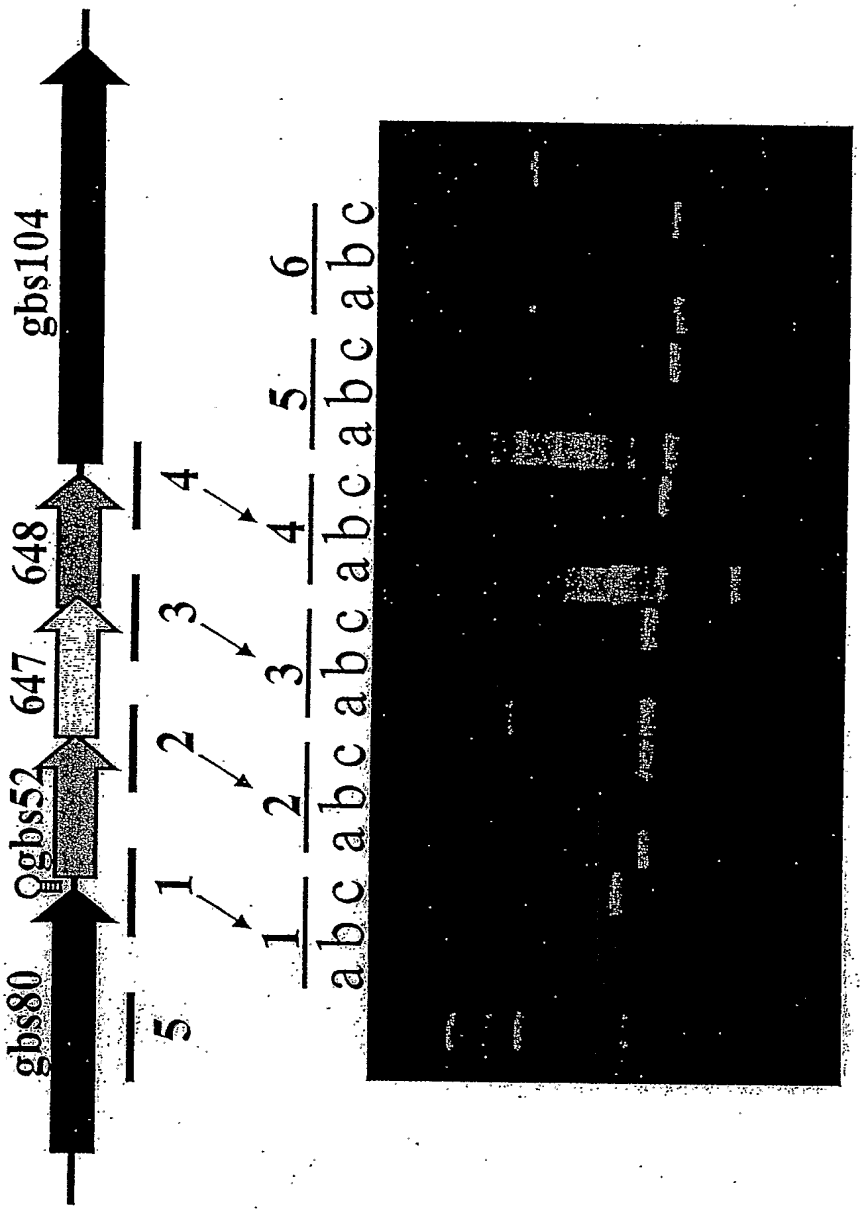


Figure 7: In frame deletions of AI-1 genes

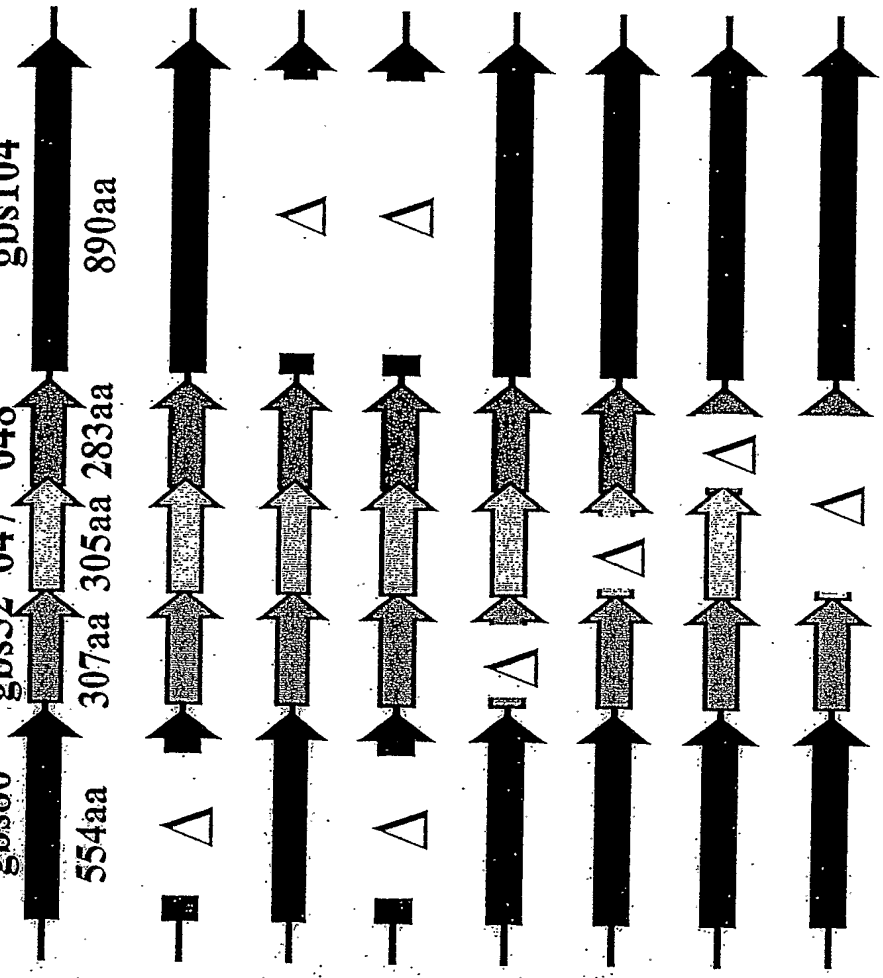


Figure 8: gbs80 is required for surface localization of gbs104

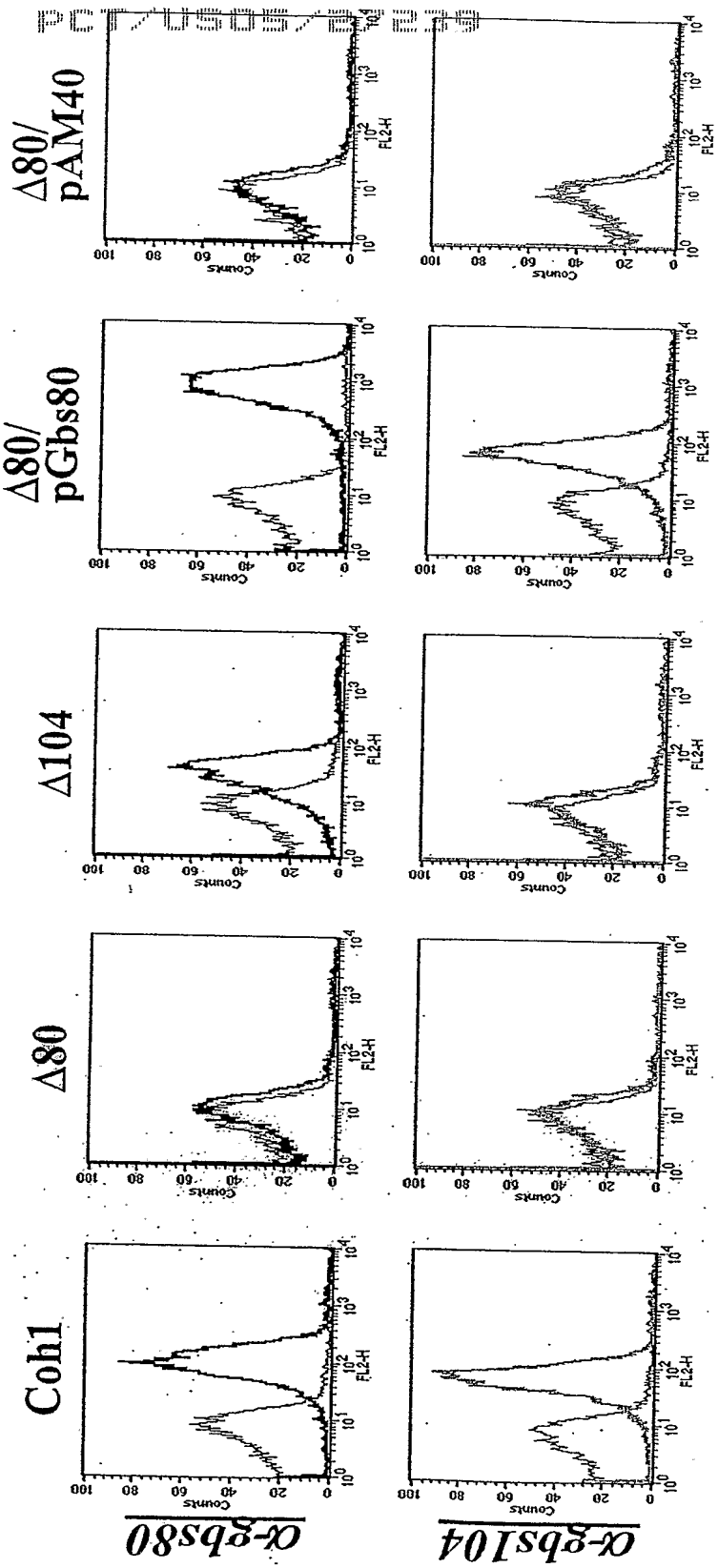


Figure 9: sortases 647 & 648 play a semi-redundant role in surface exposure of gbs80 and gbs104

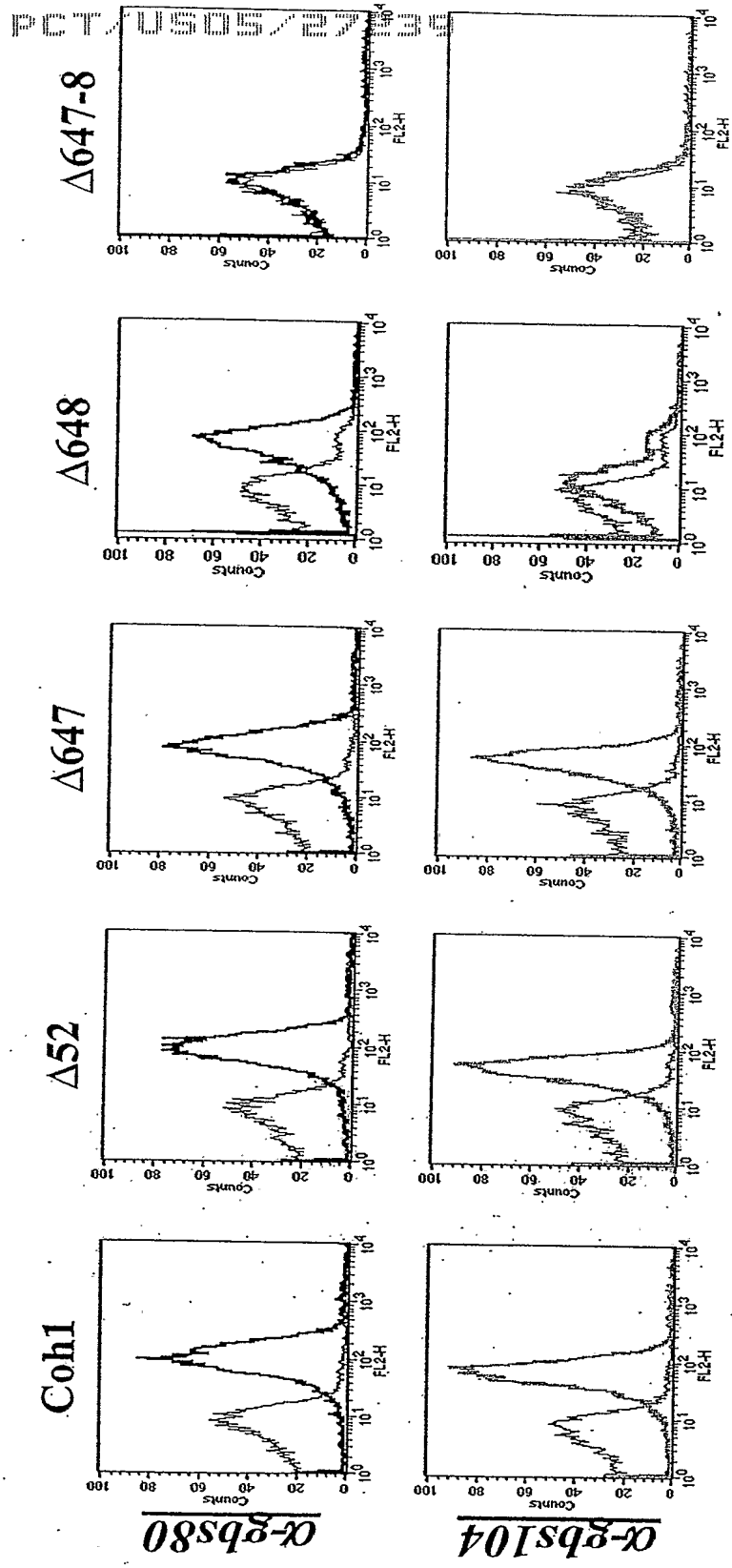
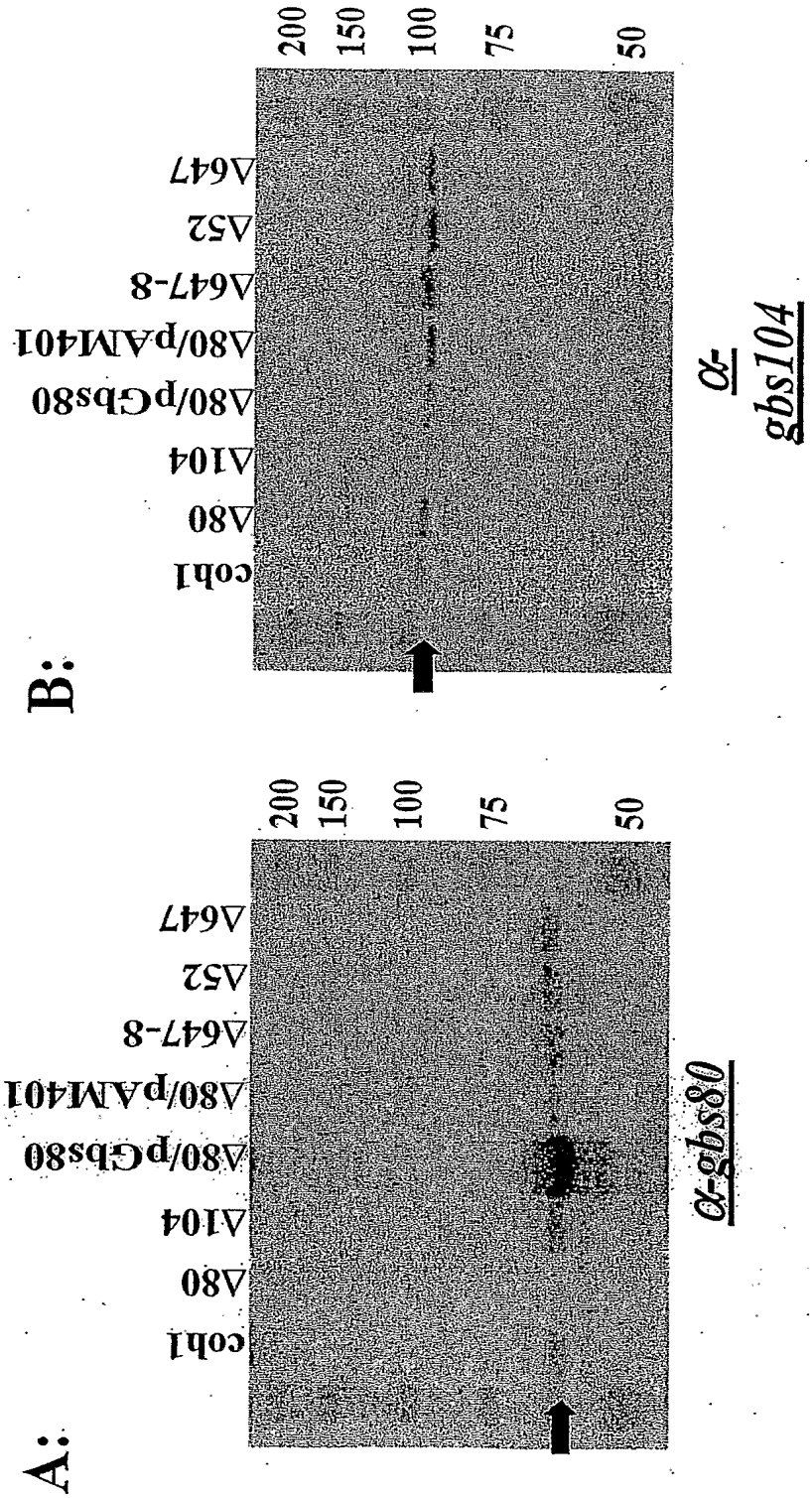


Figure 10: Western blot of mutant strains



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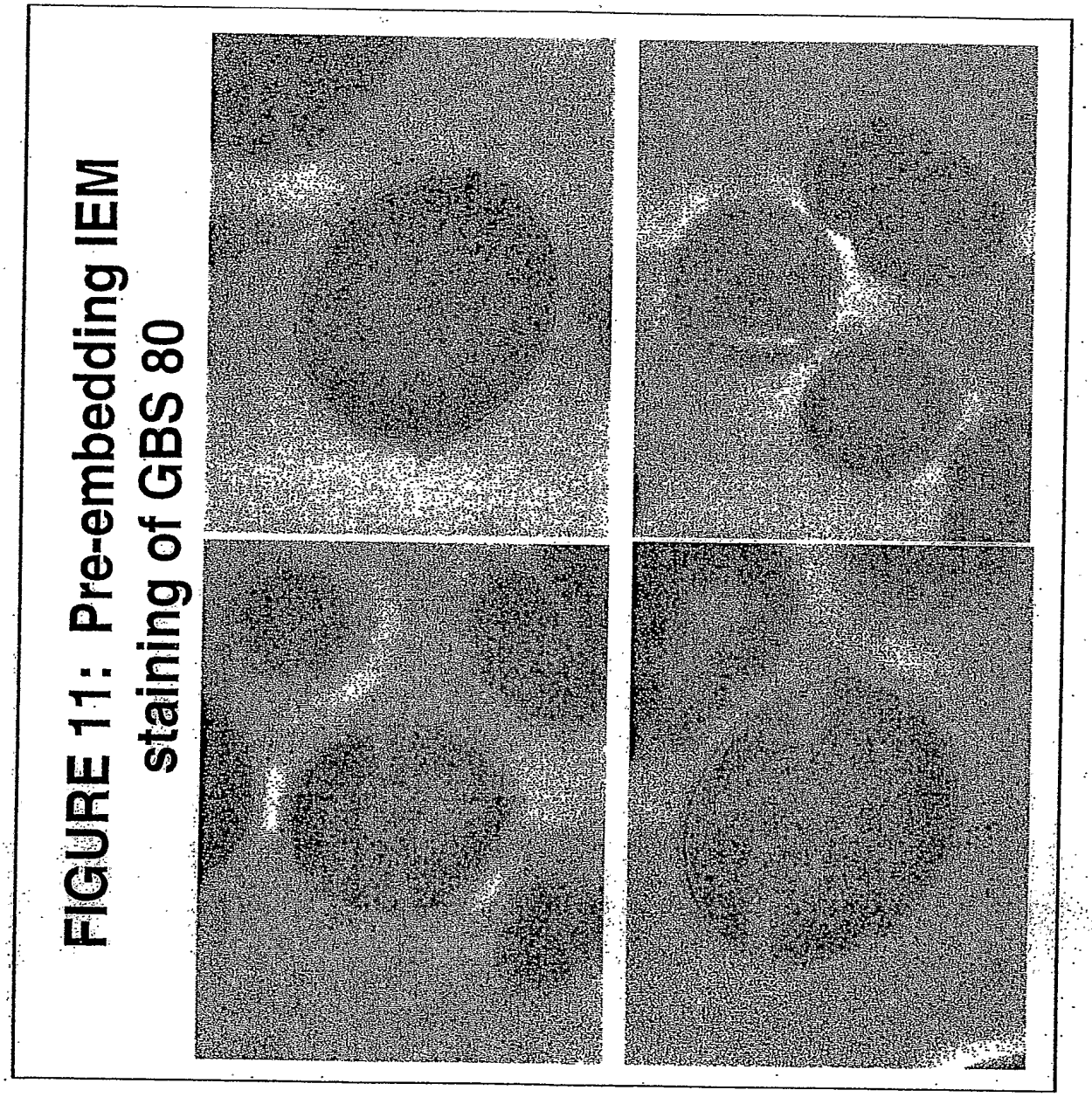

FIGURE 11: Pre-embedding IEM staining of GBS 80

FIGURE 12: Predicted Secondary Structure for GBS 067

PHD SECONDARY STRUCTURE PREDICTION for GBS 067

```
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          |         |         |         |         |         |         |
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Sequence length : 901

PHD :

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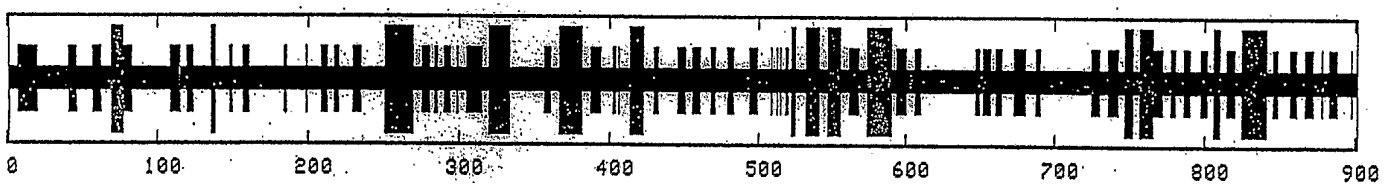
Pi helix	(Ii)	:	0 is	0.00%	Beta bridge	(Bb)	:	0 is 0.00%
Extended strand	(Ee)	:	243 is	26.97%	Beta turn	(Tt)	:	0 is 0.00%
Bend region	(Ss)	:	0 is	0.00%	Random coil	(Cc)	:	510 is 56.60%
Ambigous states	(?)	:	0 is	0.00%	Other states		:	0 is 0.00%



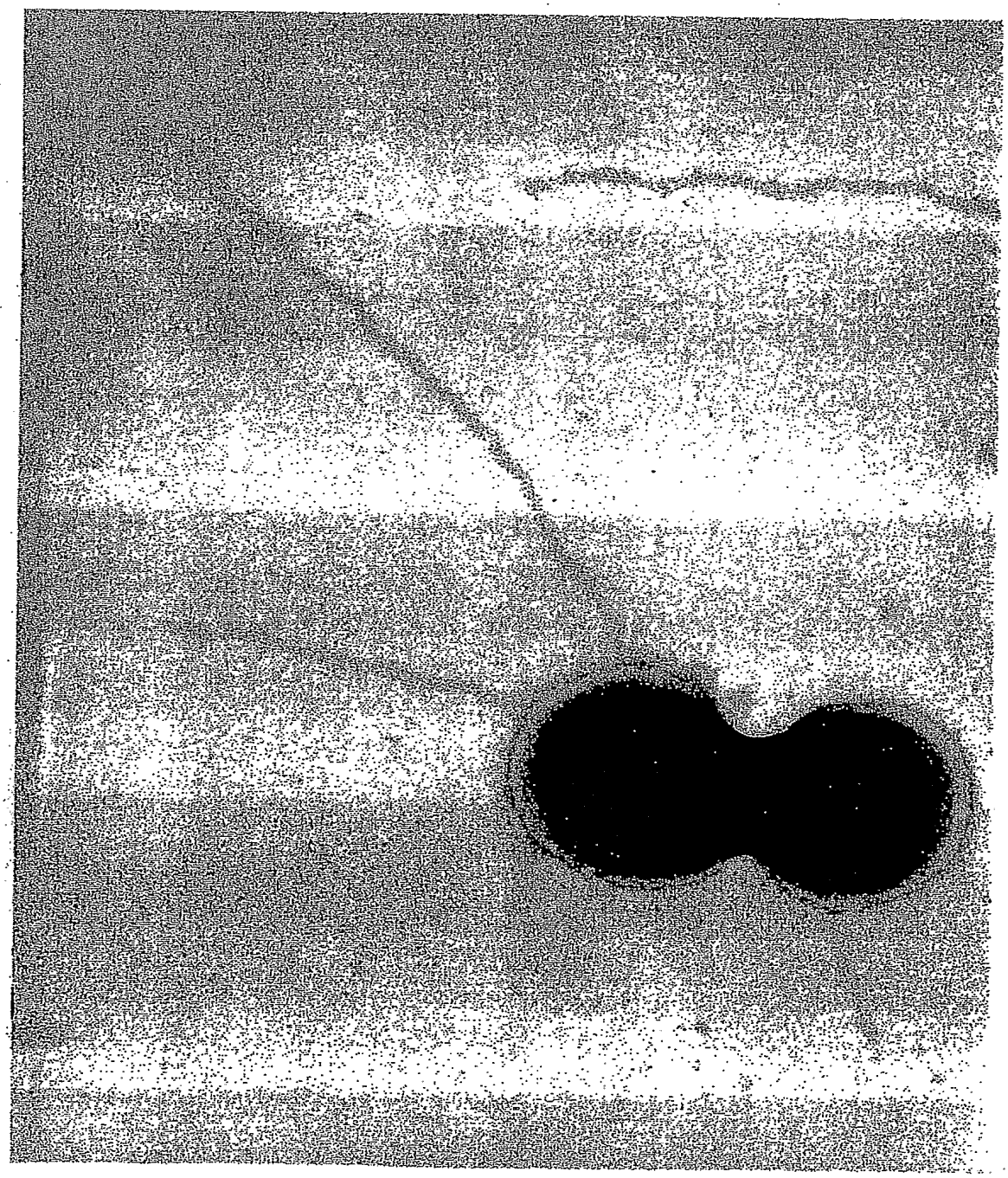


Figure 13

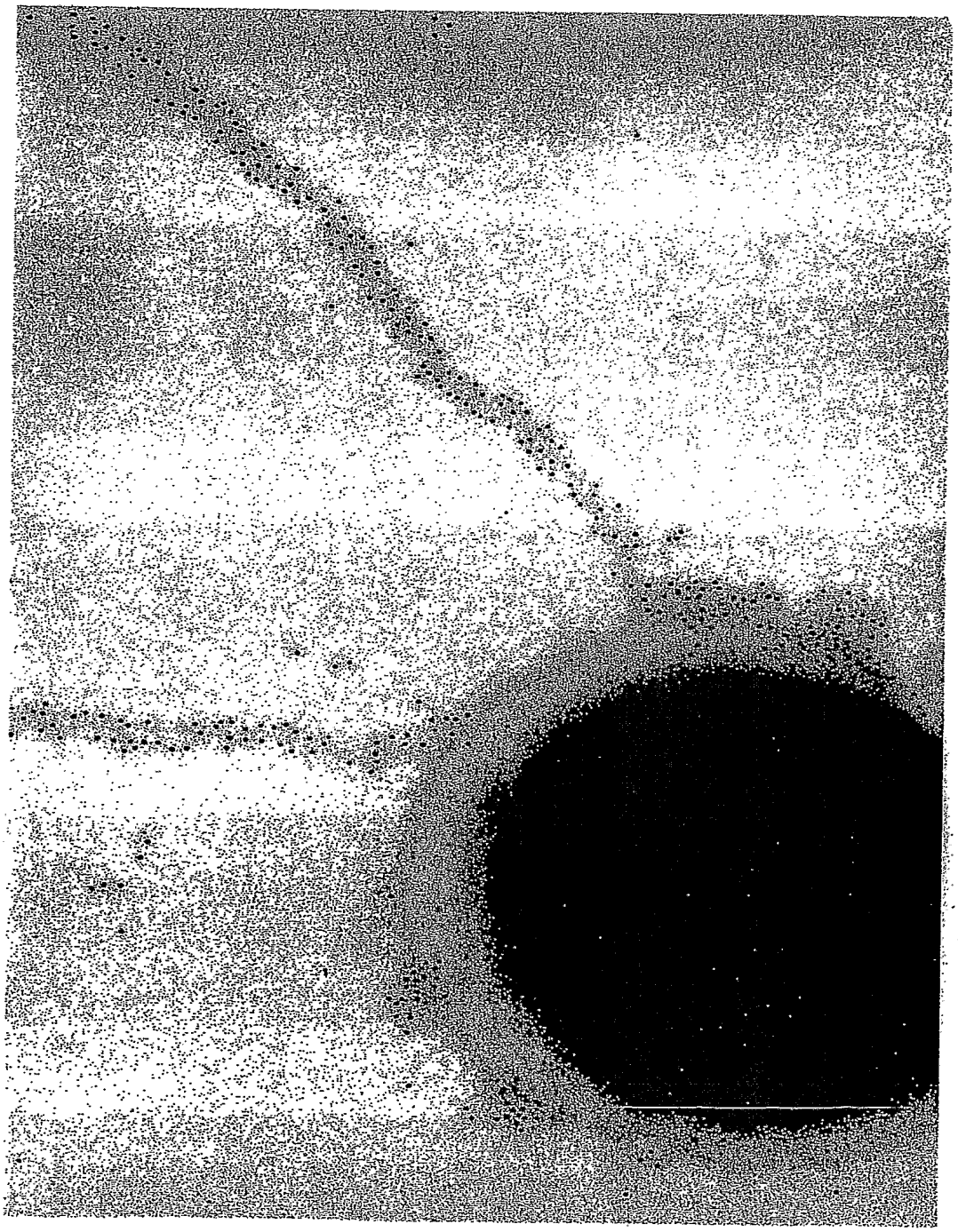


Figure 14

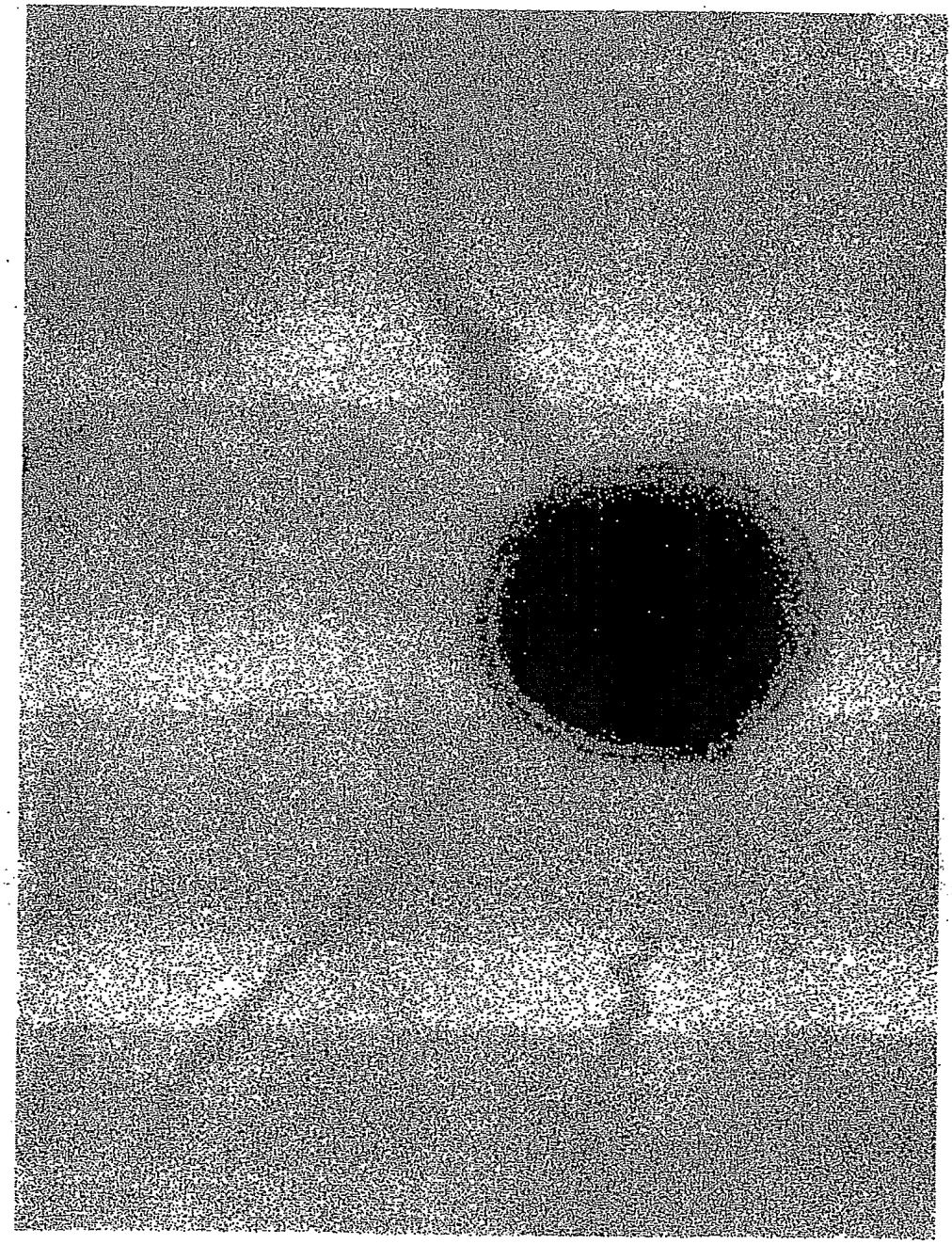


Figure 15

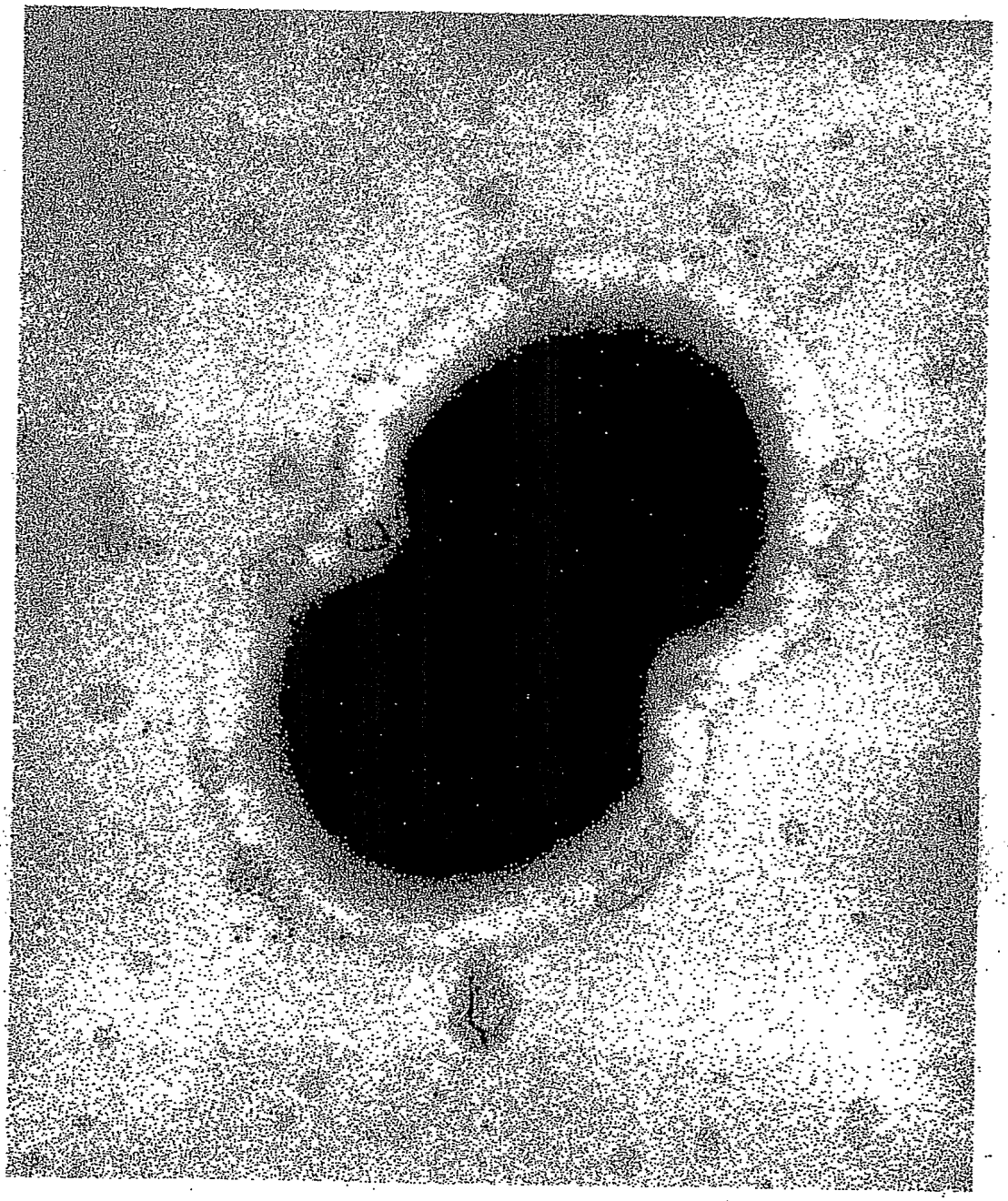


Figure 16

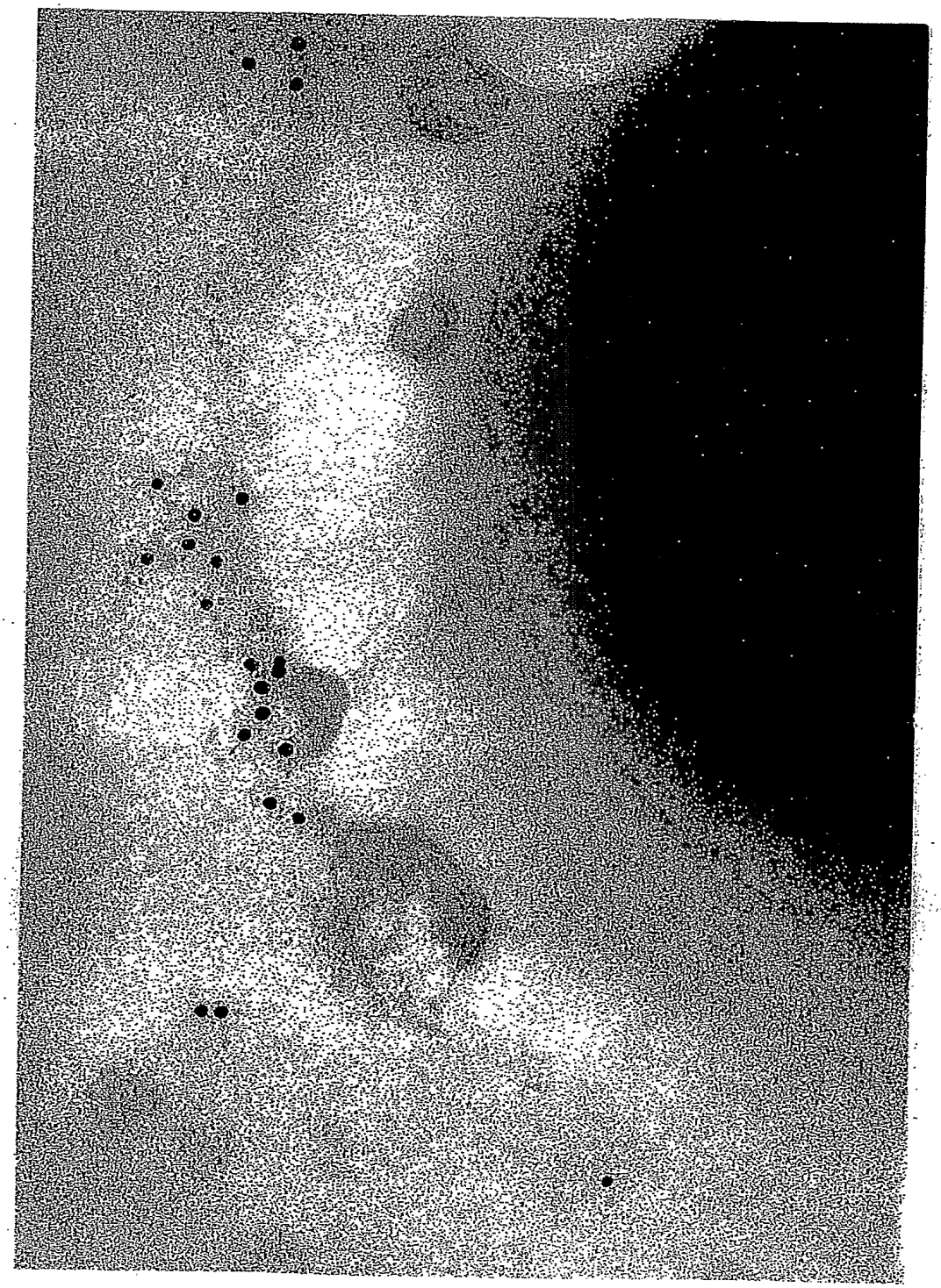


Figure 17

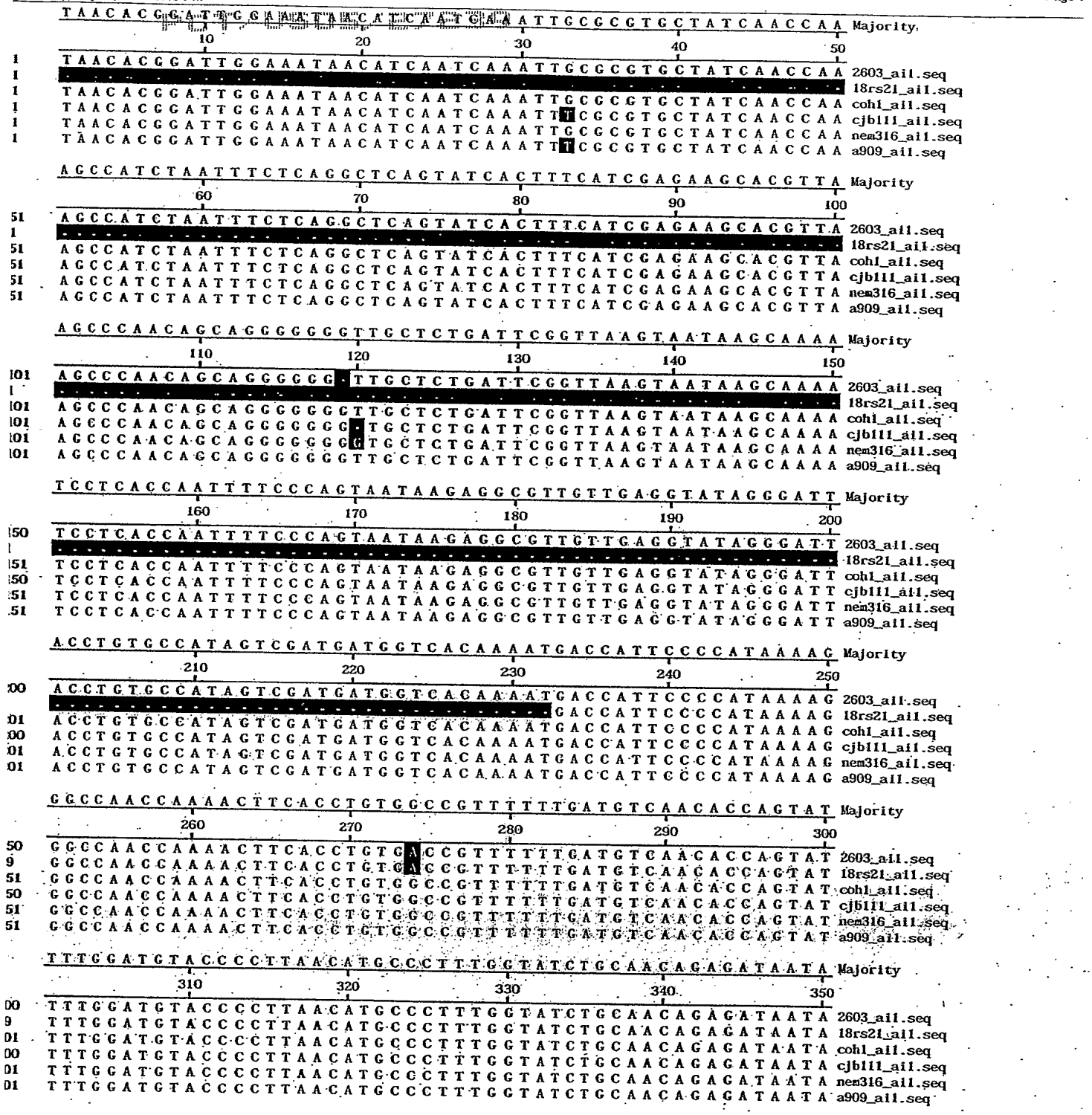

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Figure 18

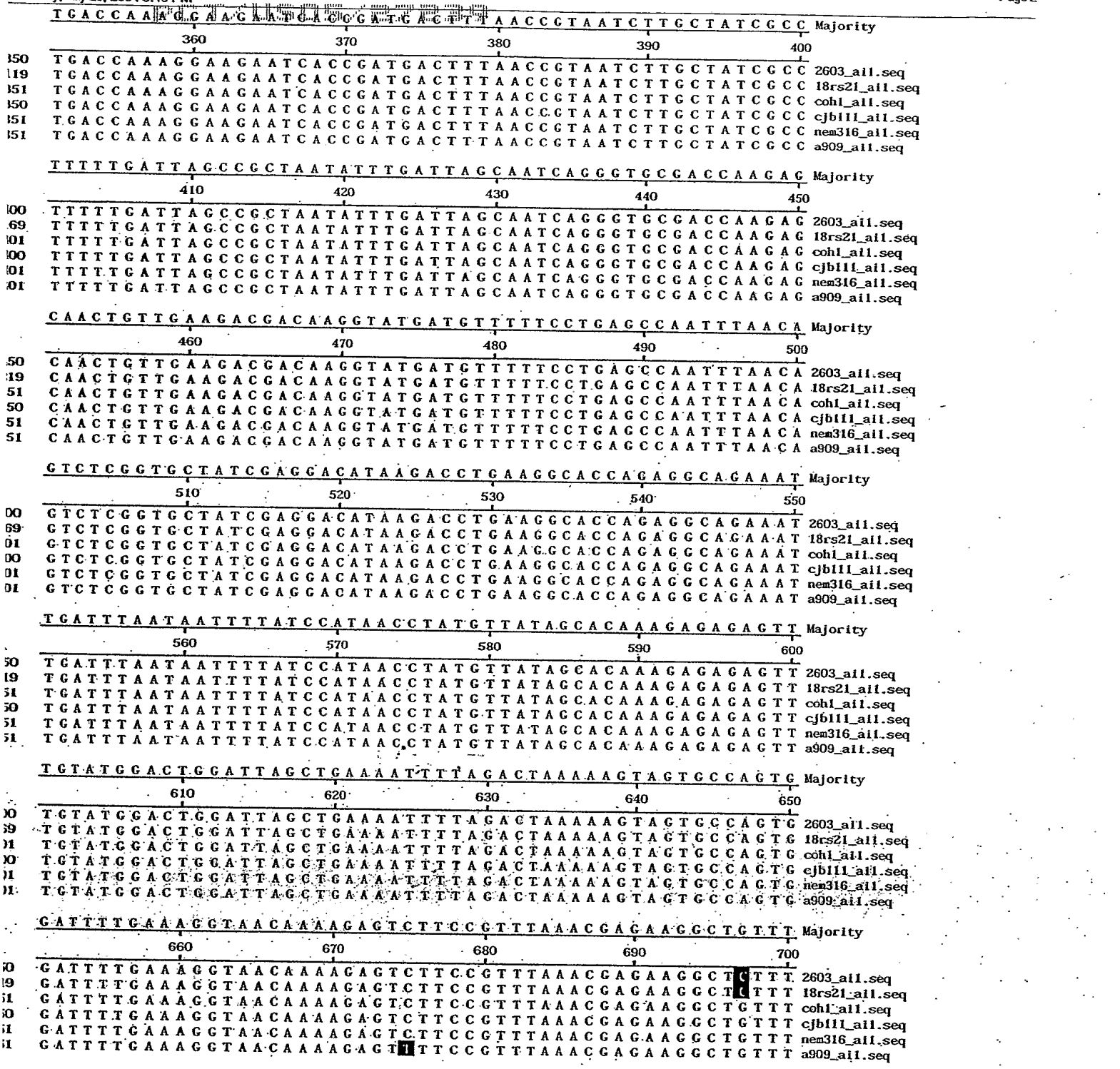
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FIGURE 18 A

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FIGURE 18 B

Alignment Report of AI-1_alignment, using J. Hein method with Weighted residue weight table.
Thursday, July 29, 2004 5:46 PM

Page 4

```
     AGGTGGTTGTCCACATAATGGAGAATACTATTGTACATTTGCTGCTTGTC Majority
              1060      1070      1080      1090      1100
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1050 AGGTGGTTGTCCACATAATGGAGAATACTATTGTACATTTGCTGCTTGTC cjb111_ai1.seq
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1100 AGAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC 2603_ai1.seq
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1101 AGAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC coh1_ai1.seq
1100 AGAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC cjb111_ai1.seq
1101 AGAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC nem316_ai1.seq
1101 AGAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC a909_ai1.seq

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1150 AGCGAATTCTTGAAACATCAATAAGATCAGGAGCCTCTTCGTTTAAAGCC 2603_ai1.seq
919  AGCGAATTCTTGAAACATCAATAAGATCAGGAGCCTCTTCGTTTAAAGCC 18rs21_ai1.seq
1151 AGCGAATTCTTGAAACATCAATAAGATCAGGAGCCTCTTCGTTTAAAGCC coh1_ai1.seq
1150 AGCGAATTCTTGAAACATCAATAAGATCAGGAGCCTCTTCGTTTAAAGCC cjb111_ai1.seq
1151 AGCGAATTCTTGAAACATCAATAAGATCAGGAGCCTATTCGTTTAAAGCC nem316_ai1.seq
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     ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTCCTC Majority
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1200 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTCCTC 2603_ai1.seq
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1200 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTTCTC cjb111_ai1.seq
1201 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTCCTC nem316_ai1.seq
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     GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT Majority
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1019 GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT 18rs21_ai1.seq
1251 GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT coh1_ai1.seq
1250 GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT cjb111_ai1.seq
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     CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGATGGGAGG Majority
              1310      1320      1330      1340      1350
1300 CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGATGGGAGG 2603_ai1.seq
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1301 CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGATGGGAGG coh1_ai1.seq
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1301 CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGATGGGAGG nem316_ai1.seq
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     CGATTAATTTCTTGCTTTAACAGTTGAGTGTTACCCAGCTTAACGAGATC Majority
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1350 CGATTAATTTCTTGCTTTAACAGTTGAGTGTTACCCAGCTTAACGAGATC 2603_ai1.seq
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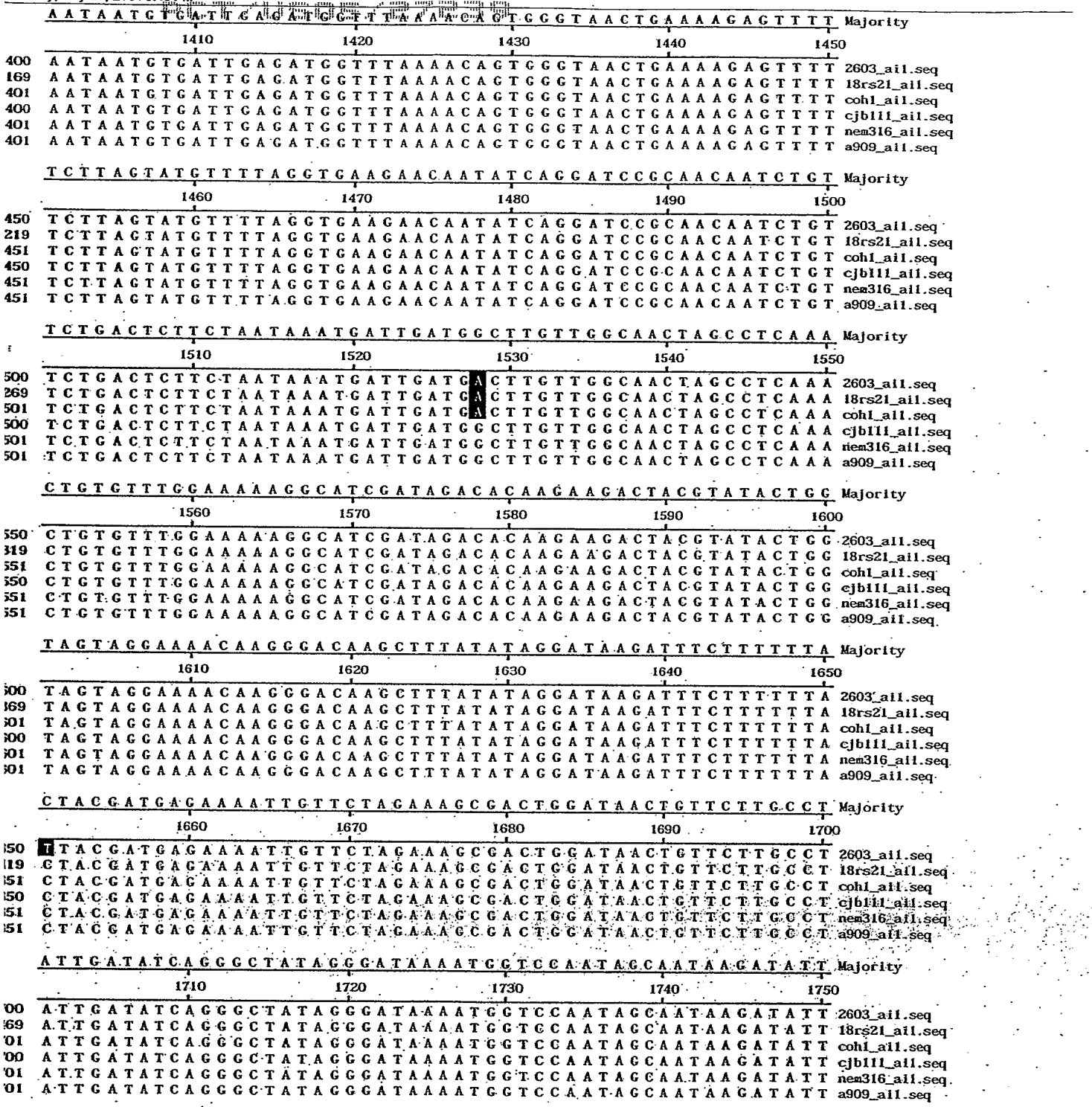
FIGURE 18 C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400 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT 2603_all.seq
169 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT 18rs21_all.seq
401 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT cohl_all.seq
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401 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT nem316_all.seq
401 AATAATGTGATTGAGATGGTTTAAAACAGTCGCTAACTGAAAAGAGTTTT a909_all.seq
TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT Majority
1460 1470 1480 1490 1500
450 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT 2603_all.seq
219 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT 18rs21_all.seq
451 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT cohl_all.seq
450 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT cjb111_all.seq
451 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT nem316_all.seq
451 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT a909_all.seq
TCTGACTCTTCTAATAAATGATTGATGGCTTGTTGGCAACTAGCCTCAAA Majority
1510 1520 1530 1540 1550
500 TCTGACTCTTCTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA 2603_all.seq
269 TCTGACTCTTCTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA 18rs21_all.seq
501 TCTGACTCTTCTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA cohl_all.seq
500 TCTGACTCTTCTAATAAATGATTGATGGCTTGTTGGCAACTAGCCTCAAA cjb111_all.seq
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1560 1570 1580 1590 1600
550 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG 2603_all.seq
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551 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG cohl_all.seq
550 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG cjb111_all.seq
551 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG nem316_all.seq
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1610 1620 1630 1640 1650
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601 TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTTA nem316_all.seq
601 TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTTA a909_all.seq
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650 CTACGATGAGAAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT cjb111_all.seq
651 CTACGATGAGAAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT nem316_all.seq
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700 ATTGATATCAGGGCTATAGGGATAAAATGGTCCAATAGCAATAAGATATT 2603_all.seq
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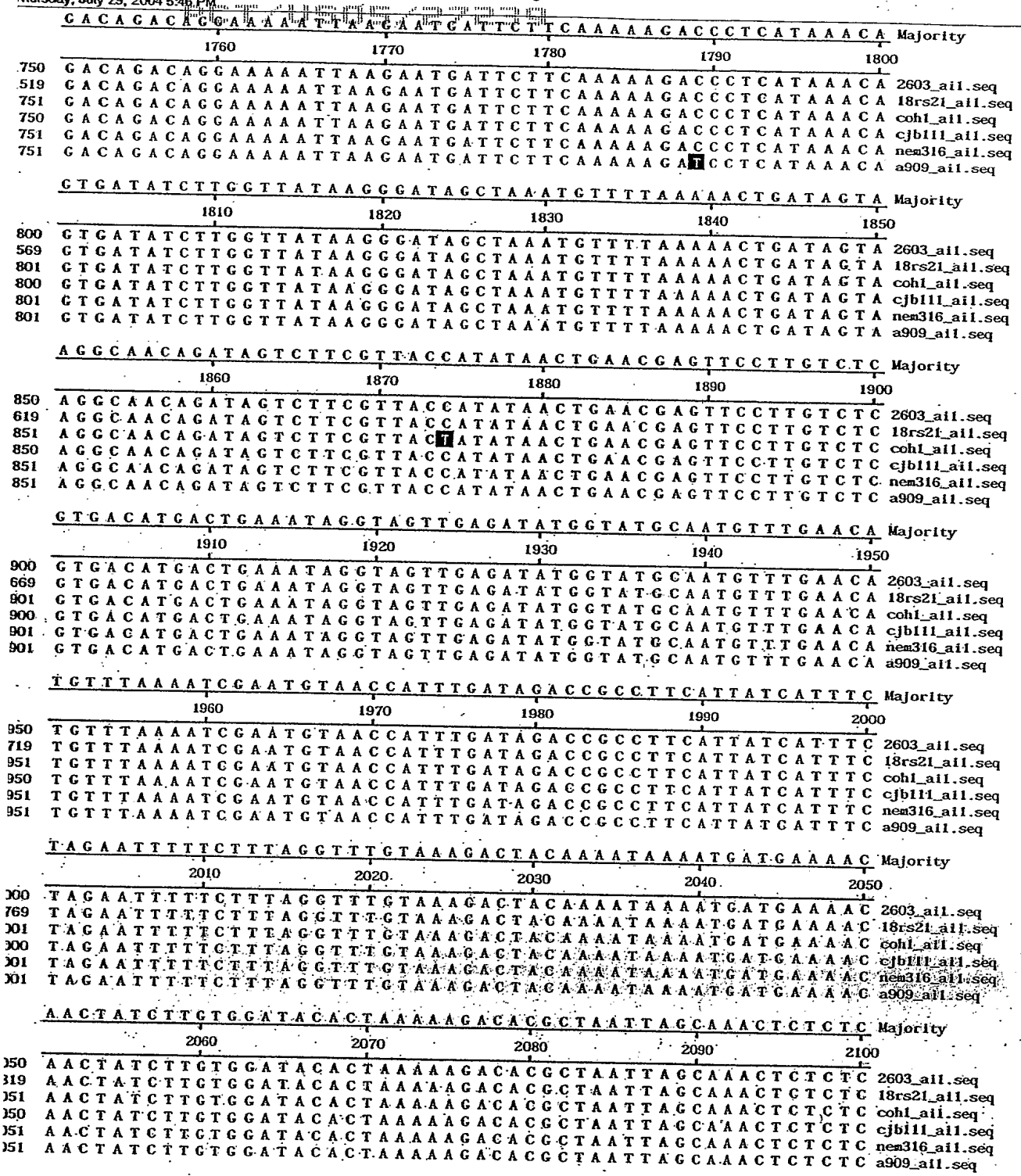
FIGURE 18 D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751 GACAGACAGGAAAAATTAAGAATGATTCTTCAAAAAGACCCTCATAAACA 18rs21_all.seq
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751 GACAGACAGGAAAAATTAAGAATGATTCTTCAAAAAGATCCTCATAAACA a909_all.seq
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1810 1820 1830 1840 1850
800 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA
569 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA 2603_all.seq
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AGGCAACAGATAGTCTTCGTTACCATATAACTGAACGAGTTCCTTGTCTC Majority
1860 1870 1880 1890 1900
850 AGGCAACAGATAGTCTTCGTTACCATATAACTGAACGAGTTCCTTGTCTC
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GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA Majority
1910 1920 1930 1940 1950
900 GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA
669 GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA 2603_all.seq
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TGTTTAAAATCGAATGTAACCATTTGATAGACCGCCTTCATTATCATTTC Majority
1960 1970 1980 1990 2000
950 TGTTTAAAATCGAATGTAACCATTTGATAGACCGCCTTCATTATCATTTC
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000 TAGAATTTTTCTTTAGGTTTGTAAAGACTACAAAATAAAATGATGAAAAC
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050 AACTATCTTGTGGATACACTAAAAAGACACGCTAATTAGCAAACTCTCTC
819 AACTATCTTGTGGATACACTAAAAAGACACGCTAATTAGCAAACTCTCTC 2603_all.seq
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FIGURE 18 E

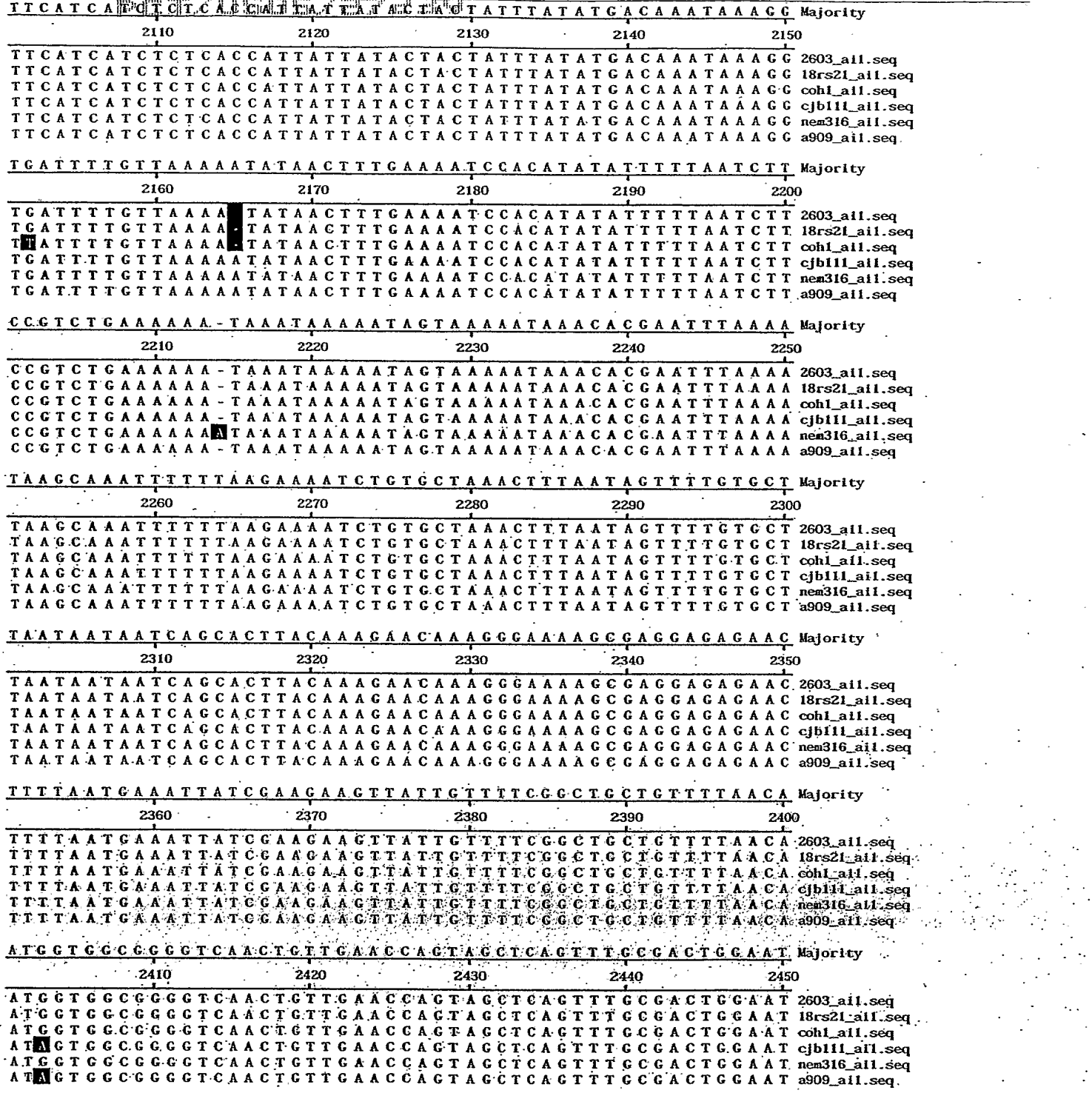
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FIGURE 18 F

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2217 CAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA 18rs21_ail.seq
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     CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT Majority
              2510      2520      2530      2540      2550
2498 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT 2603_ail.seq
2267 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT 18rs21_ail.seq
2499 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT cohl_ail.seq
2499 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT cjb111_ail.seq
2501 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT nem316_ail.seq
2500 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT a909_ail.seq

     TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC Majority
              2560      2570      2580      2590      2600
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317  TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC 18rs21_ail.seq
549  TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC cohl_ail.seq
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              2610      2620      2630      2640      2650
598  TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT 2603_ail.seq
367  TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT 18rs21_ail.seq
599  TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT cohl_ail.seq
599  TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT cjb111_ail.seq
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     ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA Majority
              2660      2670      2680      2690      2700
648  ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA 2603_ail.seq
417  ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA 18rs21_ail.seq
649  ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA cohl_ail.seq
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650  ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA a909_ail.seq

     GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG Majority
              2710      2720      2730      2740      2750
698  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG 2603_ail.seq
467  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG 18rs21_ail.seq
699  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG cohl_ail.seq
699  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG cjb111_ail.seq
701  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG nem316_ail.seq
700  GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG a909_ail.seq

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              2760      2770      2780      2790      2800
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749  TCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT cohl_ail.seq
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FIGURE 18 G

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2799 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCT coh1_all.seq
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2801 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCT nem316_all.seq
2800 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCT a909_all.seq

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                2860        2870        2880        2890        2900
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2849 TCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGT cjb111_all.seq
2851 TCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGT nem316_all.seq
2850 TCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGT a909_all.seq

TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCCTA Majority

                2910        2920        2930        2940        2950
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2899 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCCTA coh1_all.seq
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AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA Majority

                2960        2970        2980        2990        3000
2948 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA 2603_all.seq
2717 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAATAATTA 18rs21_all.seq
2949 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA coh1_all.seq
2949 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA cjb111_all.seq
2951 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA nem316_all.seq
2950 AAAACGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA a909_all.seq

GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT Majority

                3010        3020        3030        3040        3050
2998 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT 2603_all.seq
2767 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT 18rs21_all.seq
2999 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT coh1_all.seq
2999 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT cjb111_all.seq
3001 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT nem316_all.seq
3000 GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT a909_all.seq

GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA Majority

                3060        3070        3080        3090        3100
3048 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA 2603_all.seq
3017 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA 18rs21_all.seq
3049 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA coh1_all.seq
3049 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA cjb111_all.seq
3051 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA nem316_all.seq
3050 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA a909_all.seq

CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG Majority

                3110        3120        3130        3140        3150
3098 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG 2603_all.seq
3067 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG 18rs21_all.seq
3099 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG coh1_all.seq
3099 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG cjb111_all.seq
3101 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG nem316_all.seq
3100 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGCAAAAATCAAG a909_all.seq
```

FIGURE 18 H

	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	Majority
	3160 3170 3180 3190 3200	
148	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	2603_ai1.seq
917	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	18rs21_ai1.seq
149	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	coh1_ai1.seq
149	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	cjb111_ai1.seq
151	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	nem316_ai1.seq
150	A T T G G T T C G A A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C	a909_ai1.seq

	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	Majority
	3210 3220 3230 3240 3250	
198	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	2603_ai1.seq
967	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	18rs21_ai1.seq
199	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	coh1_ai1.seq
199	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	cjb111_ai1.seq
201	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	nem316_ai1.seq
200	A A C A G T T G A T A A C C A A A A T A C A T T A A A A A T T A C G T T T A A A C C A G A G A A A T	a909_ai1.seq

	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	Majority
	3260 3270 3280 3290 3300	
248	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	2603_ai1.seq
17	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	18rs21_ai1.seq
249	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	coh1_ai1.seq
249	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	cjb111_ai1.seq
251	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	nem316_ai1.seq
250	T T A A A G A A A T T G C T G A G C T A C T T A A A G G A A T G A C C C T T G T T A A A A A T C A A	a909_ai1.seq

	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	Majority
	3310 3320 3330 3340 3350	
298	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	2603_ai1.seq
67	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	18rs21_ai1.seq
299	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	coh1_ai1.seq
299	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	cjb111_ai1.seq
01	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	nem316_ai1.seq
00	G A T G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G A T G C G G C A T T T T T G G A	a909_ai1.seq

	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	Majority
	3360 3370 3380 3390 3400	
48	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	2603_ai1.seq
17	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	18rs21_ai1.seq
49	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	coh1_ai1.seq
49	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	cjb111_ai1.seq
51	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	nem316_ai1.seq
50	A A T T C C A G T T G C A T C A A C T A T T A A T G A A A A A G C A G T T T T A G G A A A A G C A A	a909_ai1.seq

	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	Majority
	3410 3420 3430 3440 3450	
98	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	2603_ai1.seq
67	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	18rs21_ai1.seq
99	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	coh1_ai1.seq
99	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	cjb111_ai1.seq
01	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	nem316_ai1.seq
00	T T G A A A A T A C T T T T G A A C T T C A A T A T G A C C A T A C T C C T G A T A A A G C T G A C	a909_ai1.seq

	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	Majority
	3460 3470 3480 3490 3500	
48	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	2603_ai1.seq
17	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	18rs21_ai1.seq
49	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	coh1_ai1.seq
49	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	cjb111_ai1.seq
51	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	nem316_ai1.seq
50	A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G	a909_ai1.seq

FIGURE 18 I

```
GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG Majority

                3510        3520        3530        3540        3550
1498 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG 2603_all.seq
1267 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG 18rs21_all.seq
1499 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG cohl_all.seq
1499 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG cjb111_all.seq
1501 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG nem316_all.seq
1500 GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG a909_all.seq

CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT Majority

                3560        3570        3580        3590        3600
1548 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT 2603_all.seq
1317 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT 18rs21_all.seq
1549 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT cohl_all.seq
1549 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT cjb111_all.seq
1551 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT nem316_all.seq
1550 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT a909_all.seq

GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT Majority

                3610        3620        3630        3640        3650
1598 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT 2603_all.seq
1367 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT 18rs21_all.seq
1599 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT cohl_all.seq
1599 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT cjb111_all.seq
1601 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT nem316_all.seq
1600 GCTCTTATTAAAGCCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT a909_all.seq

TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA Majority

                3660        3670        3680        3690        3700
1648 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA 2603_all.seq
1417 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA 18rs21_all.seq
1649 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA cohl_all.seq
1649 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA cjb111_all.seq
1651 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA nem316_all.seq
1650 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA a909_all.seq

TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA Majority

                3710        3720        3730        3740        3750
1698 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA 2603_all.seq
1467 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA 18rs21_all.seq
1699 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA cohl_all.seq
1699 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA cjb111_all.seq
1701 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA nem316_all.seq
1700 TTAAAGGTTTGGCTTATGCAGTTGATGCCGAATGCAGAGGGTACAGCAGTA a909_all.seq

ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA Majority

                3760        3770        3780        3790        3800
1748 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA 2603_all.seq
1517 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA 18rs21_all.seq
1749 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA cohl_all.seq
1749 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA cjb111_all.seq
1751 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA nem316_all.seq
1750 ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA a909_all.seq

TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA Majority

                3810        3820        3830        3840        3850
1798 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA 2603_all.seq
1567 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA 18rs21_all.seq
1799 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA cohl_all.seq
1799 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA cjb111_all.seq
1801 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA nem316_all.seq
1800 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA a909_all.seq
```

FIGURE 18 J


Majority
2603_all.seq
18rs21_all.seq
coh1_all.seq
cjb111_all.seq
nem316_all.seq
a909_all.seq

FIGURE 18 K

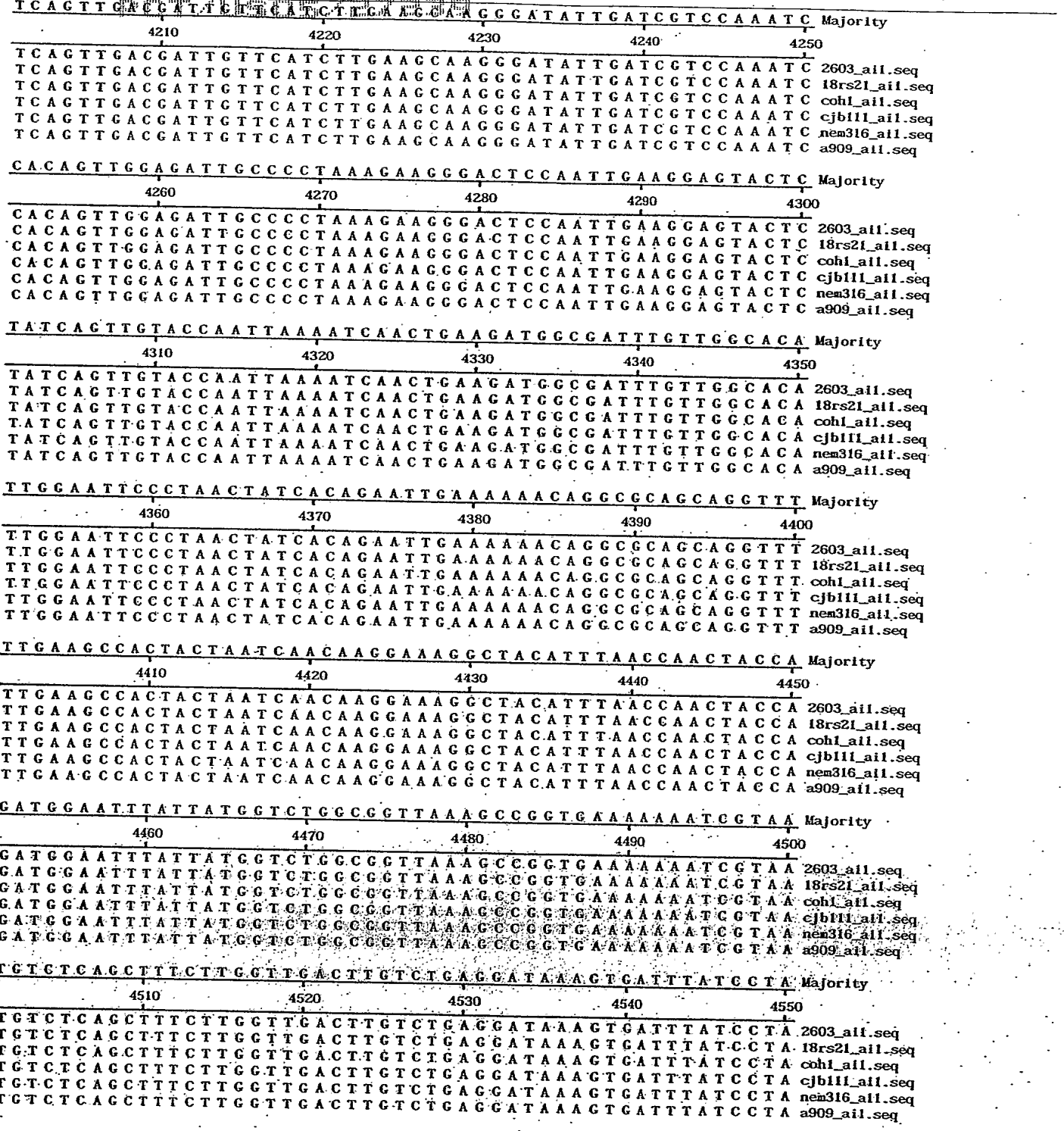
Majority
4210 4220 4230 4240 4250
4198 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC
3967 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC 2603_all.seq
4199 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC 18rs21_all.seq
4199 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC coh1_all.seq
4201 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC cjb111_all.seq
4200 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC nem316_all.seq
a909_all.seq
Majority
4260 4270 4280 4290 4300
4248 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC
4017 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC 2603_all.seq
4249 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC 18rs21_all.seq
4249 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC coh1_all.seq
4251 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC cjb111_all.seq
4250 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC nem316_all.seq
a909_all.seq
Majority
4310 4320 4330 4340 4350
4298 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA
4067 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA 2603_all.seq
4299 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA 18rs21_all.seq
4299 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA coh1_all.seq
4301 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA cjb111_all.seq
4300 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA nem316_all.seq
a909_all.seq
Majority
4360 4370 4380 4390 4400
4348 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT
4117 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT 2603_all.seq
4349 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT 18rs21_all.seq
4349 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT coh1_all.seq
4351 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT cjb111_all.seq
4350 TTGGAATTCCCTAACTATCACAGAATTGAAAAAAACAGGCGCAGCAGGTTT nem316_all.seq
a909_all.seq
Majority
4410 4420 4430 4440 4450
4398 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA
4167 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA 2603_all.seq
4399 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA 18rs21_all.seq
4399 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA coh1_all.seq
4401 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA cjb111_all.seq
4400 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA nem316_all.seq
a909_all.seq
Majority
4460 4470 4480 4490 4500
4448 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA
4217 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA 2603_all.seq
4449 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA 18rs21_all.seq
4449 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA coh1_all.seq
4451 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA cjb111_all.seq
4450 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAAATCGTAA nem316_all.seq
a909_all.seq
Majority
4510 4520 4530 4540 4550
4498 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA
4267 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA 2603_all.seq
4499 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA 18rs21_all.seq
4499 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA coh1_all.seq
4501 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA cjb111_all.seq
4500 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA nem316_all.seq
a909_all.seq

FIGURE 18 L

```
     AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT Majority
              4560      4570      4580      4590      4600
4548 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT 2603_ail.seq
4317 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT 18rs21_ail.seq
4549 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT cohl_ail.seq
4549 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT cjb111_ail.seq
4551 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT nem316_ail.seq
4550 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT a909_ail.seq

     GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA Majority
              4610      4620      4630      4640      4650
4598 GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA 2603_ail.seq
4367 GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA 18rs21_ail.seq
4599 GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA cohl_ail.seq
4599 GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA cjb111_ail.seq
4601 GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA nem316_ail.seq
4600 GGTGATACCAAAAAAACACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA a909_ail.seq

     GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA Majority
              4660      4670      4680      4690      4700
4648 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA 2603_ail.seq
4417 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA 18rs21_ail.seq
4649 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA cohl_ail.seq
4649 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA cjb111_ail.seq
4651 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA nem316_ail.seq
4650 GAATGGTAGGACTCCTATTCGTGTGAAAAATGGGGTGCATTCTCAAGATA a909_ail.seq

     TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT Majority
              4710      4720      4730      4740      4750
4698 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT 2603_ail.seq
4467 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT 18rs21_ail.seq
4699 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT cohl_ail.seq
4699 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT cjb111_ail.seq
4701 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT nem316_ail.seq
4700 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT a909_ail.seq

     TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC Majority
              4760      4770      4780      4790      4800
4748 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC 2603_ail.seq
4517 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC 18rs21_ail.seq
4749 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC cohl_ail.seq
4749 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC cjb111_ail.seq
4751 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC nem316_ail.seq
4750 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC a909_ail.seq

     AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA Majority
              4810      4820      4830      4840      4850
4798 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA 2603_ail.seq
4567 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA 18rs21_ail.seq
4799 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA cohl_ail.seq
4799 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA cjb111_ail.seq
4801 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA nem316_ail.seq
4800 AGGATATCAGATCGGACAGGCAGAGACTGCTGTGACTATTGAAAAATCAA a909_ail.seq

     AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG Majority
              4860      4870      4880      4890      4900
4848 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG 2603_ail.seq
4617 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG 18rs21_ail.seq
4849 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG cohl_ail.seq
4849 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG cjb111_ail.seq
4851 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG nem316_ail.seq
4850 AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG a909_ail.seq
```

FIGURE 18 M

```
     C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C Majority
               4910                4920                4930                4940                4950
4898 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C 2603_ai1.seq
4667 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C 18rs21_ai1.seq
4899 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C coh1_ai1.seq
4899 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C cjb111_ai1.seq
4901 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C nem316_ai1.seq
4900 C C A T C T C G A G G A G C T C T T A T T C C C A A A A C A G G T G A G C A A C A G G C A A T G G C a909_ai1.seq

     A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T Majority
               4960                4970                4980                4990                5000
4948 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T 2603_ai1.seq
4717 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T 18rs21_ai1.seq
4949 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T coh1_ai1.seq
4949 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T cjb111_ai1.seq
4951 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T nem316_ai1.seq
4950 A C T T G T A A T T A T T G G T G G T A T T T T A A T T G C T T T A G C C T T A C G A T T A C T A T a909_ai1.seq

     C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A Majority
               5010                5020                5030                5040                5050
4998 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A 2603_ai1.seq
4767 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A 18rs21_ai1.seq
4999 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A coh1_ai1.seq
4999 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A cjb111_ai1.seq
5001 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A nem316_ai1.seq
5000 C A A A A C A T C G G A A A C A T C A A A A T A A G G A T T A G C A T G G G A C A A A A A T C A A A a909_ai1.seq

     A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T Majority
               5060                5070                5080                5090                5100
5048 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T 2603_ai1.seq
4817 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T 18rs21_ai1.seq
5049 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T coh1_ai1.seq
5049 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T cjb111_ai1.seq
5051 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T nem316_ai1.seq
5050 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T a909_ai1.seq

     T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C Majority
               5110                5120                5130                5140                5150
5098 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C 2603_ai1.seq
4867 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C 18rs21_ai1.seq
5099 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C coh1_ai1.seq
5099 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C cjb111_ai1.seq
5101 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C nem316_ai1.seq
5100 T A G C G G G T T T C C T T G T T T T G G C A T T T C C C A T C G T T A G T C A G G T C A T G T A C a909_ai1.seq

     T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A Majority
               5160                5170                5180                5190                5200
148  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A 2603_ai1.seq
917  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A 18rs21_ai1.seq
149  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A coh1_ai1.seq
149  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A cjb111_ai1.seq
151  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A nem316_ai1.seq
150  T T T C A A G C C T C T C A C G C C A A T A T T A A T G C T T T T A A A G A A G C T G T T A C C A A a909_ai1.seq

     G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A Majority
               5210                5220                5230                5240                5250
198  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A 2603_ai1.seq
967  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A 18rs21_ai1.seq
199  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A coh1_ai1.seq
199  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A cjb111_ai1.seq
201  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A nem316_ai1.seq
200  G A T T G A C C G G G T G G A G A T T A A T C G G C G T T T A G A A C T T G C T T A T G C T T A T A a909_ai1.seq
```

FIGURE 18 N

```
                ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA Majority
                         5260      5270      5280      5290      5300
5248 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA 2603_all.seq
5017 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA 18rs21_all.seq
5249 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA cohl_all.seq
5249 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA cjb111_all.seq
5251 ACGCCAGTATAGCACGTGCCAAAACTAATGGCGAATATTCAGCGCTTAAA nem316_all.seq
5250 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA a909_all.seq

                GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG Majority
                         5310      5320      5330      5340      5350
5298 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG 2603_all.seq
5067 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG 18rs21_all.seq
5299 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG cohl_all.seq
5299 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG cjb111_all.seq
5301 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG nem316_all.seq
5300 GACCCCTACTCTGCTGAACAAAAGCAGGCAGGGGTCGTTGAGTACGCCCG a909_all.seq

                CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA Majority
                         5360      5370      5380      5390      5400
5348 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA 2603_all.seq
5117 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA 18rs21_all.seq
5349 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA cohl_all.seq
5349 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA cjb111_all.seq
5351 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA nem316_all.seq
5350 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA a909_all.seq

                ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG Majority
                         5410      5420      5430      5440      5450
5398 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG 2603_all.seq
5167 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG 18rs21_all.seq
5399 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG cohl_all.seq
5399 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG cjb111_all.seq
5401 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG nem316_all.seq
5400 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAAATCTTCAGAGG a909_all.seq

                GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC Majority
                         5460      5470      5480      5490      5500
448 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC 2603_all.seq
217 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC 18rs21_all.seq
449 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC cohl_all.seq
449 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC cjb111_all.seq
451 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC nem316_all.seq
450 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC a909_all.seq

                TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA Majority
                         5510      5520      5530      5540      5550
498 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA 2603_all.seq
267 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA 18rs21_all.seq
499 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA cohl_all.seq
499 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA cjb111_all.seq
501 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA nem316_all.seq
500 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA a909_all.seq

                CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC Majority
                         5560      5570      5580      5590      5600
548 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC 2603_all.seq
317 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC 18rs21_all.seq
549 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC cohl_all.seq
549 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC cjb111_all.seq
551 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC nem316_all.seq
550 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC a909_all.seq
```

FIGURE 18 O

```
      GGCGGAATGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA Majority

                5610        5620        5630        5640        5650
598   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA 2603_all.seq
367   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA 18rs21_all.seq
599   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA cohl_all.seq
599   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA cjb111_all.seq
601   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA nem316_all.seq
600   GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA a909_all.seq

      TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT Majority

                5660        5670        5680        5690        5700
648   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT 2603_all.seq
417   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT 18rs21_all.seq
649   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT cohl_all.seq
649   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT cjb111_all.seq
651   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT nem316_all.seq
650   TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT a909_all.seq

      TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC Majority

                5710        5720        5730        5740        5750
698   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC 2603_all.seq
467   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC 18rs21_all.seq
699   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC cohl_all.seq
699   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC cjb111_all.seq
701   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC nem316_all.seq
700   TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC a909_all.seq

      AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT Majority

                5760        5770        5780        5790        5800
748   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT 2603_all.seq
517   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT 18rs21_all.seq
749   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT cohl_all.seq
749   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT cjb111_all.seq
751   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT nem316_all.seq
750   AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT a909_all.seq

      CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA Majority

                5810        5820        5830        5840        5850
798   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA 2603_all.seq
567   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA 18rs21_all.seq
799   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA cohl_all.seq
799   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA cjb111_all.seq
801   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA nem316_all.seq
800   CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA a909_all.seq

      TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG Majority

                5860        5870        5880        5890        5900
848   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG 2603_all.seq
617   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG 18rs21_all.seq
849   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG cohl_all.seq
849   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG cjb111_all.seq
851   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG nem316_all.seq
850   TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAAGCGG a909_all.seq

      AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA Majority

                5910        5920        5930        5940        5950
898   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA 2603_all.seq
667   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA 18rs21_all.seq
899   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA cohl_all.seq
899   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA cjb111_all.seq
901   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA nem316_all.seq
900   AGAAAGAATGAAAAAGCGGCTAGTCAAAATAGTCACAATAATTCGAAATA a909_all.seq
```

FIGURE 18 P

```
     ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT Majority
                5960      5970      5980      5990      6000
5948 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT 2603_ai1.seq
5717 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT 18rs21_ai1.seq
5949 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT coh1_ai1.seq
5949 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT cjb111_ai1.seq
5951 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT nem316_ai1.seq
5950 ATAAAATCAGAACCCTCATTTTTGTGATGGGAAGTCTGATTCTCTTATTT a909_ai1.seq

     CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA Majority
                6010      6020      6030      6040      6050
5998 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA 2603_ai1.seq
5767 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA 18rs21_ai1.seq
5999 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA coh1_ai1.seq
5999 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA cjb111_ai1.seq
6001 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA nem316_ai1.seq
6000 CCGATTGTGAGCCAGGTAAGTTACTACCTTGCTTCGCATCAAAATATTAA a909_ai1.seq

     TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC Majority
                6060      6070      6080      6090      6100
6048 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC 2603_ai1.seq
5817 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC 18rs21_ai1.seq
6049 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC coh1_ai1.seq
6049 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC cjb111_ai1.seq
6051 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC nem316_ai1.seq
6050 TCAATTTAAGCGGGAAGTCGCTAAGATTGATACTAATACGGTTGAACGAC a909_ai1.seq

     GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG Majority
                6110      6120      6130      6140      6150
6098 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG 2603_ai1.seq
5867 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG 18rs21_ai1.seq
6099 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG coh1_ai1.seq
6099 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG cjb111_ai1.seq
6101 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG nem316_ai1.seq
6100 GCATCGCTTTAGCTAATGCTTACAATGAGACGTTATCAAGGAATCCCTTG a909_ai1.seq

     CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC Majority
                6160      6170      6180      6190      6200
148  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC 2603_ai1.seq
917  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC 18rs21_ai1.seq
149  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC coh1_ai1.seq
149  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC cjb111_ai1.seq
151  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC nem316_ai1.seq
150  CTTATAGACCCTTTTACCAGTAAGCAAAAAGAAGGTTTGAGAGAGTATGC a909_ai1.seq

     TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA Majority
                6210      6220      6230      6240      6250
198  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA 2603_ai1.seq
967  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA 18rs21_ai1.seq
199  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA coh1_ai1.seq
199  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA cjb111_ai1.seq
201  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA nem316_ai1.seq
200  TCGTATGCTTGAAGTTCATGAGCAAATAGGTCATGTGGCAATCCCAAGTA a909_ai1.seq

     TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG Majority
                6260      6270      6280      6290      6300
248  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG 2603_ai1.seq
017  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG 18rs21_ai1.seq
249  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG coh1_ai1.seq
249  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG cjb111_ai1.seq
251  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG nem316_ai1.seq
250  TTGCGGTTGATATTCCAATTTATGCTGGAACATCCGAAACTGTGCTTCAG a909_ai1.seq
```

FIGURE 18 Q

```
AAAGGTACTGCGCGATTTGCAGCGAACCGACTCTTCCAGTGCGAGGTTTGTC Majority
                6310        6320        6330        6340        6350
6298 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC 2603_all.seq
6067 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC 18rs21_all.seq
6299 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC cohl_all.seq
6299 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC cjb111_all.seq
6301 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC nem316_all.seq
6300 AAAGGTAGTGGCCATTTGGAGCGAACCAGTCTTCCAGTGCGAGGTTTGTC a909_all.seq

AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT Majority
                6360        6370        6380        6390        6400
6348 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT 2603_all.seq
6117 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT 18rs21_all.seq
6349 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT cohl_all.seq
6349 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT cjb111_all.seq
6351 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT nem316_all.seq
6350 AACCCATTCAGTACTAACTGCCCACCGTGCCTTGCCAACAGCTAGGCTAT a909_all.seq

TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC Majority
                6410        6420        6430        6440        6450
6398 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC 2603_all.seq
6167 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC 18rs21_all.seq
6399 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC cohl_all.seq
6399 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC cjb111_all.seq
6401 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC nem316_all.seq
6400 TTACCGACTTAAATAAAGTTAAAAAAAGGCCAGATTTTCTATGTGACGAAC a909_all.seq

ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC Majority
                6460        6470        6480        6490        6500
6448 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC 2603_all.seq
6217 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC 18rs21_all.seq
6449 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC cohl_all.seq
6449 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC cjb111_all.seq
6451 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC nem316_all.seq
6450 ATCAAGGAAACACTTGCCTACAAAGTCGTGTCTATCAAAGTTGTGGATCC a909_all.seq

AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT Majority
                6510        6520        6530        6540        6550
6498 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT 2603_all.seq
6267 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT 18rs21_all.seq
6499 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT cohl_all.seq
6499 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT cjb111_all.seq
6501 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT nem316_all.seq
6500 AACAGCTTTAAGTGAGGTTAAGATTGTCAATGGTAAGGATTATATAACCT a909_all.seq

TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA Majority
                6560        6570        6580        6590        6600
6548 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA 2603_all.seq
6317 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA 18rs21_all.seq
6549 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA cohl_all.seq
6549 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA cjb111_all.seq
6551 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA nem316_all.seq
6550 TGCTGACTTGCACACCTTACATGATCAATAGTCATCGTCTCTTGGTAAAA a909_all.seq

GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA Majority
                6610        6620        6630        6640        6650
6598 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA 2603_all.seq
6367 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA 18rs21_all.seq
6599 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA cohl_all.seq
6599 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA cjb111_all.seq
6601 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA nem316_all.seq
6600 GGAGAGCGTATTCCTTATGATTCTACCGAGCCGGAAAAGCACAAAGAACA a909_all.seq
```

FIGURE 18 R

```
      AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT Majority
               6660      6670      6680      6690      6700
648   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT 2603_all.seq
417   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT 18rs21_all.seq
649   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT cohl_all.seq
649   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT cjb111_all.seq
651   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT nem316_all.seq
650   AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT a909_all.seq

      TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT Majority
               6710      6720      6730      6740      6750
698   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT 2603_all.seq
467   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT 18rs21_all.seq
699   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT cohl_all.seq
699   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT cjb111_all.seq
701   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT nem316_all.seq
700   TATTAATTGGACTCTTCATCGTGATAATGATGAGAAGATGGATGCAACAT a909_all.seq

      CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT Majority
               6760      6770      6780      6790      6800
748   CGTCAATAACGATGTTGTGAATGGCTTACTT----ATCAAATAGGTGACT 2603_all.seq
517   CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT 18rs21_all.seq
749   CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT cohl_all.seq
749   CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT cjb111_all.seq
751   CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT nem316_all.seq
750   CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT a909_all.seq

      AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA Majority
               6810      6820      6830      6840      6850
794   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA 2603_all.seq
567   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA 18rs21_all.seq
799   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA cohl_all.seq
799   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA cjb111_all.seq
801   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA nem316_all.seq
800   AATGATGATTGTGAATAATGGTTATCTAGAAGGGAGAAAAATGAAAAAGA a909_all.seq

      GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA Majority
               6860      6870      6880      6890      6900
844   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA 2603_all.seq
617   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA 18rs21_all.seq
849   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA cohl_all.seq
849   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA cjb111_all.seq
851   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA nem316_all.seq
850   GACAAAAAATATGGAGAGGGTTATCAGTTACTTTACTAATCCTGTCCCAA a909_all.seq

      ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC Majority
               6910      6920      6930      6940      6950
894   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC 2603_all.seq
667   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC 18rs21_all.seq
899   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC cohl_all.seq
899   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC cjb111_all.seq
901   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC nem316_all.seq
900   ATTCCATTTGGTATATTGGTACAAGGTGAAACCCAAGATACCAATCAAGC a909_all.seq

      ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG Majority
               6960      6970      6980      6990      7000
944   ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG 2603_all.seq
717   ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG 18rs21_all.seq
949   ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG cohl_all.seq
949   ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG cjb111_all.seq
951   ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG nem316_all.seq
950   ACTTGGAAAAGTAATTGTTAAAAAAACGGGGGACAATGCTACACCATTAG a909_all.seq
```

FIGURE 18 S

```
GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT Majority

          7010      7020      7030      7040      7050
6994 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT 2603_all.seq
5767 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT 18rs21_all.seq
6999 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT cohl_all.seq
6999 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT cjbill_all.seq
7001 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT nem316_all.seq
7000 GCAAAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGT a909_all.seq

CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC Majority

          7060      7070      7080      7090      7100
7044 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC 2603_all.seq
6817 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC 18rs21_all.seq
7049 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC cohl_all.seq
7049 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC cjbill_all.seq
7051 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC nem316_all.seq
7050 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC a909_all.seq

TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA Majority

          7110      7120      7130      7140      7150
7094 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA 2603_all.seq
6867 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA 18rs21_all.seq
7099 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA cohl_all.seq
7099 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA cjbill_all.seq
7101 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA nem316_all.seq
7100 TGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGTTATAAAAAAA a909_all.seq

CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC Majority

          7160      7170      7180      7190      7200
7144 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC 2603_all.seq
6917 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC 18rs21_all.seq
7149 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC cohl_all.seq
7149 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC cjbill_all.seq
7151 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC nem316_all.seq
7150 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC a909_all.seq

GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC Majority

          7210      7220      7230      7240      7250
7194 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC 2603_all.seq
6967 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC 18rs21_all.seq
7199 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC cohl_all.seq
7199 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC cjbill_all.seq
7201 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC nem316_all.seq
7200 GAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAGTTTTGAATGC a909_all.seq

CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT Majority

          7260      7270      7280      7290      7300
7244 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT 2603_all.seq
7017 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT 18rs21_all.seq
7249 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT cohl_all.seq
7249 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT cjbill_all.seq
7251 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT nem316_all.seq
7250 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAAATTACCCAT a909_all.seq

TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT Majority

          7310      7320      7330      7340      7350
7294 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT 2603_all.seq
7067 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT 18rs21_all.seq
7299 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT cohl_all.seq
7299 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT cjbill_all.seq
7301 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT nem316_all.seq
7300 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT a909_all.seq
```

FIGURE 18T

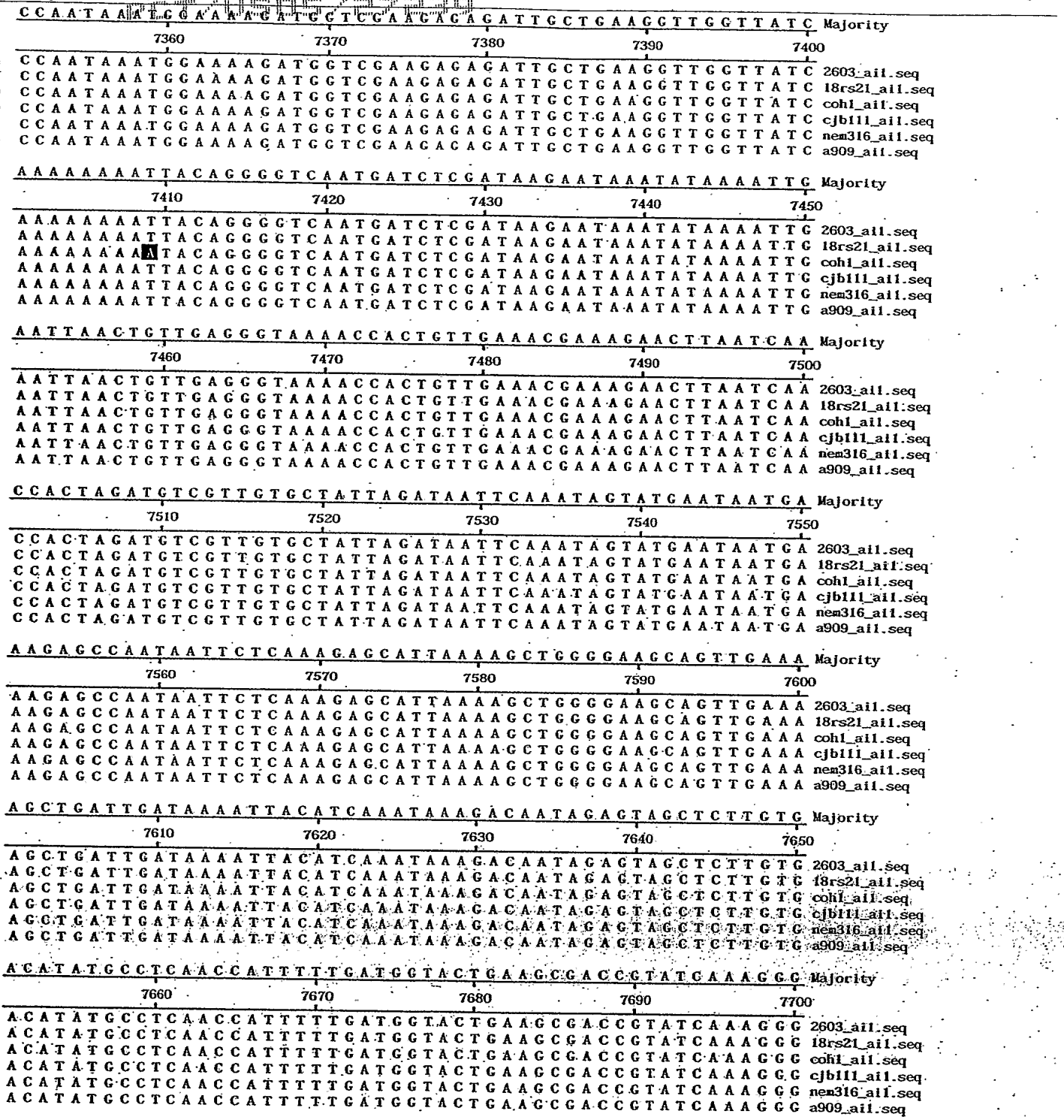
CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC Majority
7360 7370 7380 7390 7400
7344 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC 2603_all.seq
7117 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC 18rs21_all.seq
7349 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC cohl_all.seq
7349 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC cjb111_all.seq
7351 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATC nem316_all.seq
7350 CCAATAAATGGAAAAGATGGTCGAAGACACAGATTGCTGAAGGTTGGTTATC a909_all.seq
AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG Majority
7410 7420 7430 7440 7450
7394 AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG 2603_all.seq
7167 AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG 18rs21_all.seq
7399 AAAAAAAAATACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG cohl_all.seq
7399 AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG cjb111_all.seq
7401 AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG nem316_all.seq
7400 AAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTG a909_all.seq
AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA Majority
7460 7470 7480 7490 7500
7444 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA 2603_all.seq
7217 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA 18rs21_all.seq
7449 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA cohl_all.seq
7449 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA cjb111_all.seq
7451 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA nem316_all.seq
7450 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA a909_all.seq
CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA Majority
7510 7520 7530 7540 7550
7494 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA 2603_all.seq
7267 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA 18rs21_all.seq
7499 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA cohl_all.seq
7499 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA cjb111_all.seq
7501 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA nem316_all.seq
7500 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA a909_all.seq
AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA Majority
7560 7570 7580 7590 7600
544 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA 2603_all.seq
317 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA 18rs21_all.seq
549 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA cohl_all.seq
549 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA cjb111_all.seq
551 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA nem316_all.seq
550 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA a909_all.seq
AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG Majority
7610 7620 7630 7640 7650
594 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG 2603_all.seq
367 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG 18rs21_all.seq
599 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG cohl_all.seq
599 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG cjb111_all.seq
601 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG nem316_all.seq
600 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG a909_all.seq
ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG Majority
7660 7670 7680 7690 7700
644 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG 2603_all.seq
417 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG 18rs21_all.seq
649 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG cohl_all.seq
649 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG cjb111_all.seq
651 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG nem316_all.seq
650 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG a909_all.seq

FIGURE 18 U


AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT Majority
7710 7720 7730 7740 7750
7694 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT 2603_all.seq
7467 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT 18rs21_all.seq
7699 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT cohl_all.seq
7699 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT cjb111_all.seq
7701 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT nem316_all.seq
7700 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT a909_all.seq
ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT Majority
7760 7770 7780 7790 7800
7744 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT 2603_all.seq
7517 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT 18rs21_all.seq
7749 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT cohl_all.seq
7749 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT cjb111_all.seq
7751 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT nem316_all.seq
7750 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT a909_all.seq
TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA Majority
7810 7820 7830 7840 7850
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7567 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA 18rs21_all.seq
7799 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA cohl_all.seq
7799 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA cjb111_all.seq
7801 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA nem316_all.seq
7800 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA a909_all.seq
GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA Majority
7860 7870 7880 7890 7900
7844 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA 2603_all.seq
7617 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA 18rs21_all.seq
7849 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA cohl_all.seq
7849 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA cjb111_all.seq
7851 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA nem316_all.seq
7850 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA a909_all.seq
CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA Majority
7910 7920 7930 7940 7950
7894 CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA 2603_all.seq
7667 CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA 18rs21_all.seq
7899 CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA cohl_all.seq
7899 CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA cjb111_all.seq
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AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC Majority
7960 7970 7980 7990 8000
7944 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC 2603_all.seq
7717 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC 18rs21_all.seq
7949 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC cohl_all.seq
7949 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC cjb111_all.seq
7951 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC nem316_all.seq
7950 AGTTCTAATGCTAGAAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC a909_all.seq
TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC Majority
8010 8020 8030 8040 8050
7994 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC 2603_all.seq
7767 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC 18rs21_all.seq
7999 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC cohl_all.seq
7999 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC cjb111_all.seq
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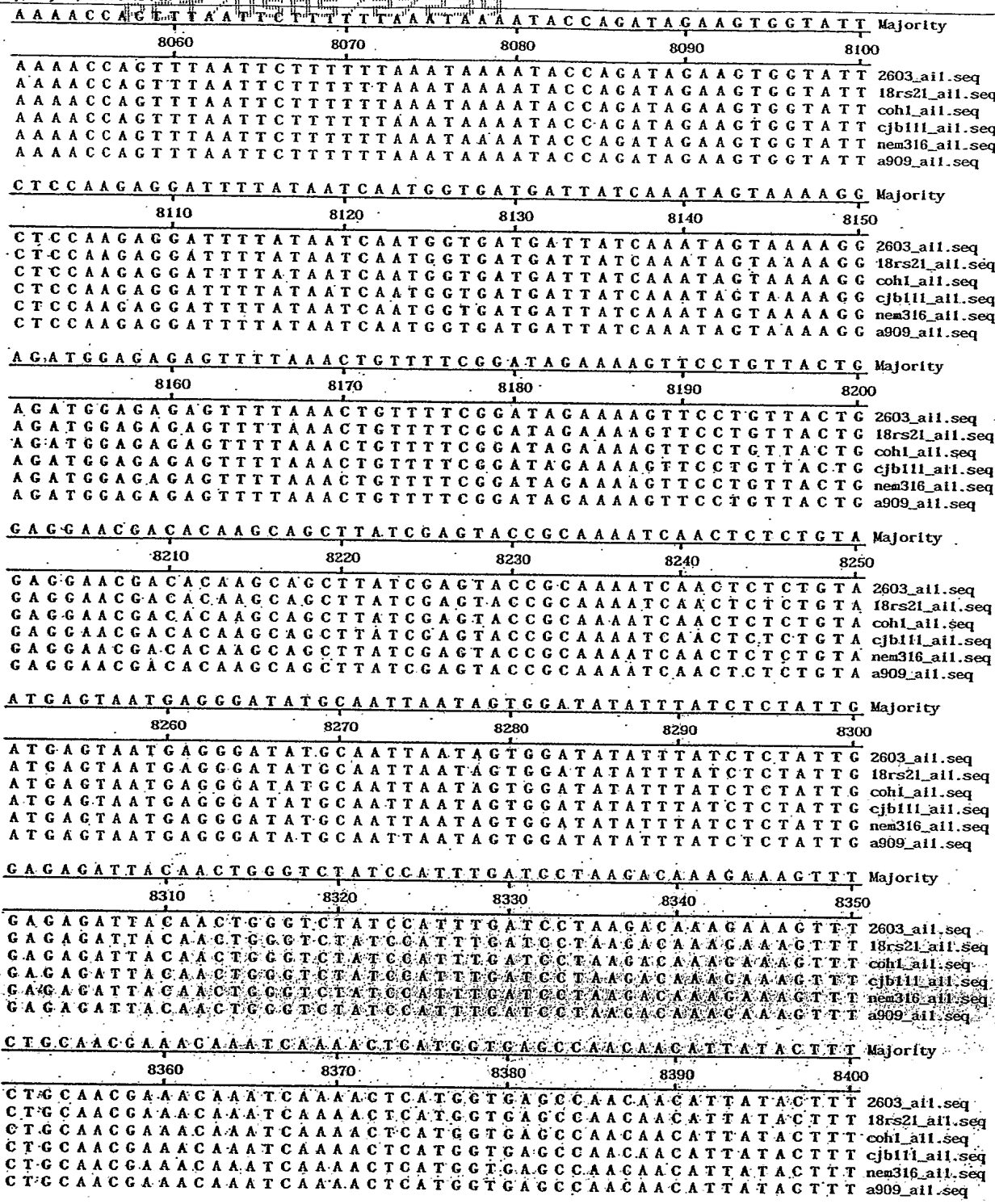
FIGURE 18 V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8049 AAAACCAGTTTAATTCTTTTTTAAATAAAATACCAGATAGAAGTGGTATT coh1_all.seq
8049 AAAACCAGTTTAATTCTTTTTTAAATAAAATACCAGATAGAAGTGGTATT cjb111_all.seq
8051 AAAACCAGTTTAATTCTTTTTTAAATAAAATACCAGATAGAAGTGGTATT nem316_all.seq
8050 AAAACCAGTTTAATTCTTTTTTAAATAAAATACCAGATAGAAGTGGTATT a909_all.seq
CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG Majority
8110 8120 8130 8140 8150
8094 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG 2603_all.seq
7867 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG 18rs21_all.seq
8099 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG coh1_all.seq
8099 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG cjb111_all.seq
8101 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG nem316_all.seq
8100 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG a909_all.seq
AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG Majority
8160 8170 8180 8190 8200
8144 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG 2603_all.seq
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8149 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG coh1_all.seq
8149 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG cjb111_all.seq
8151 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG nem316_all.seq
8150 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTG a909_all.seq
GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA Majority
8210 8220 8230 8240 8250
8194 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA 2603_all.seq
7967 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA 18rs21_all.seq
8199 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA coh1_all.seq
8199 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA cjb111_all.seq
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ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG Majority
8260 8270 8280 8290 8300
8244 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG 2603_all.seq
8017 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG 18rs21_all.seq
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GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT Majority
8310 8320 8330 8340 8350
8294 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT 2603_all.seq
8067 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT 18rs21_all.seq
8299 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT coh1_all.seq
8299 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT cjb111_all.seq
8301 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTT nem316_all.seq
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CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAACAACATTATACTTT Majority
8360 8370 8380 8390 8400
8344 CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAACAACATTATACTTT 2603_all.seq
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8349 CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAACAACATTATACTTT coh1_all.seq
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FIGURE 18 W

```
      AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG Majority
          8410      8420      8430      8440      8450
8394  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG 2603_ai1.seq
8167  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG 18rs21_ai1.seq
8399  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG coh1_ai1.seq
8399  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG cjb111_ai1.seq
8401  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG nem316_ai1.seq
8400  AATGCAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGCATTGG a909_ai1.seq

      TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC Majority
          8460      8470      8480      8490      8500
8444  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC 2603_ai1.seq
8217  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC 18rs21_ai1.seq
8449  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC coh1_ai1.seq
8449  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC cjb111_ai1.seq
8451  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC nem316_ai1.seq
8450  TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC a909_ai1.seq

      AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT Majority
          8510      8520      8530      8540      8550
8494  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT 2603_ai1.seq
8267  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT 18rs21_ai1.seq
3499  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT coh1_ai1.seq
8499  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT cjb111_ai1.seq
3501  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT nem316_ai1.seq
3500  AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT a909_ai1.seq

      AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA Majority
          8560      8570      8580      8590      8600
3544  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA 2603_ai1.seq
3317  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA 18rs21_ai1.seq
3549  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA coh1_ai1.seq
3549  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA cjb111_ai1.seq
3551  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA nem316_ai1.seq
3550  AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA a909_ai1.seq

      ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG Majority
          8610      8620      8630      8640      8650
3594  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG 2603_ai1.seq
3367  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG 18rs21_ai1.seq
3599  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG coh1_ai1.seq
3599  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG cjb111_ai1.seq
i601  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG nem316_ai1.seq
i600  ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG a909_ai1.seq

      AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTG Majority
          8660      8670      8680      8690      8700
i644  AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTG 2603_ai1.seq
i417  AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTG 18rs21_ai1.seq
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i651  AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTG nem316_ai1.seq
i650  AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTG a909_ai1.seq

      GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC Majority
          8710      8720      8730      8740      8750
i694  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC 2603_ai1.seq
i467  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC 18rs21_ai1.seq
i699  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC coh1_ai1.seq
i699  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC cjb111_ai1.seq
i701  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC nem316_ai1.seq
i700  GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC a909_ai1.seq
```

FIGURE 18 X

```
     AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA Majority
              8760      8770      8780      8790      8800
8744 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA 2603_all.seq
8517 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA 18rs21_all.seq
8749 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA coh1_all.seq
8749 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA cjb111_all.seq
8751 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA nem316_all.seq
8750 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA a909_all.seq

     CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA Majority
              8810      8820      8830      8840      8850
8794 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA 2603_all.seq
8567 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA 18rs21_all.seq
8799 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA coh1_all.seq
8799 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA cjb111_all.seq
8801 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA nem316_all.seq
8800 CATCTCAAACCATCAAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA a909_all.seq

     GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA Majority
              8860      8870      8880      8890      8900
8844 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA 2603_all.seq
8617 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA 18rs21_all.seq
8849 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA coh1_all.seq
8849 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA cjb111_all.seq
8851 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA nem316_all.seq
8850 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA a909_all.seq

     ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG Majority
              8910      8920      8930      8940      8950
8894 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG 2603_all.seq
8667 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG 18rs21_all.seq
8899 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG coh1_all.seq
8899 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG cjb111_all.seq
8901 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG nem316_all.seq
8900 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG a909_all.seq

     AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT Majority
              8960      8970      8980      8990      9000
8944 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT 2603_all.seq
8717 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT 18rs21_all.seq
8949 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT coh1_all.seq
8949 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT cjb111_all.seq
8951 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT nem316_all.seq
8950 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT a909_all.seq

     GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA Majority
              9010      9020      9030      9040      9050
8994 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA 2603_all.seq
8767 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA 18rs21_all.seq
8999 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA coh1_all.seq
8999 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA cjb111_all.seq
9001 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA nem316_all.seq
9000 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGA a909_all.seq

     ATTTATTAAAGTTAATAAAGACAAACATTCAGAATCGCTTTTGGGAGCTA Majority
              9060      9070      9080      9090      9100
9044 ATTTATTAAAGTTAATAAAGACAAACATTCAGAATCGCTTTTGGGAGCTA 2603_all.seq
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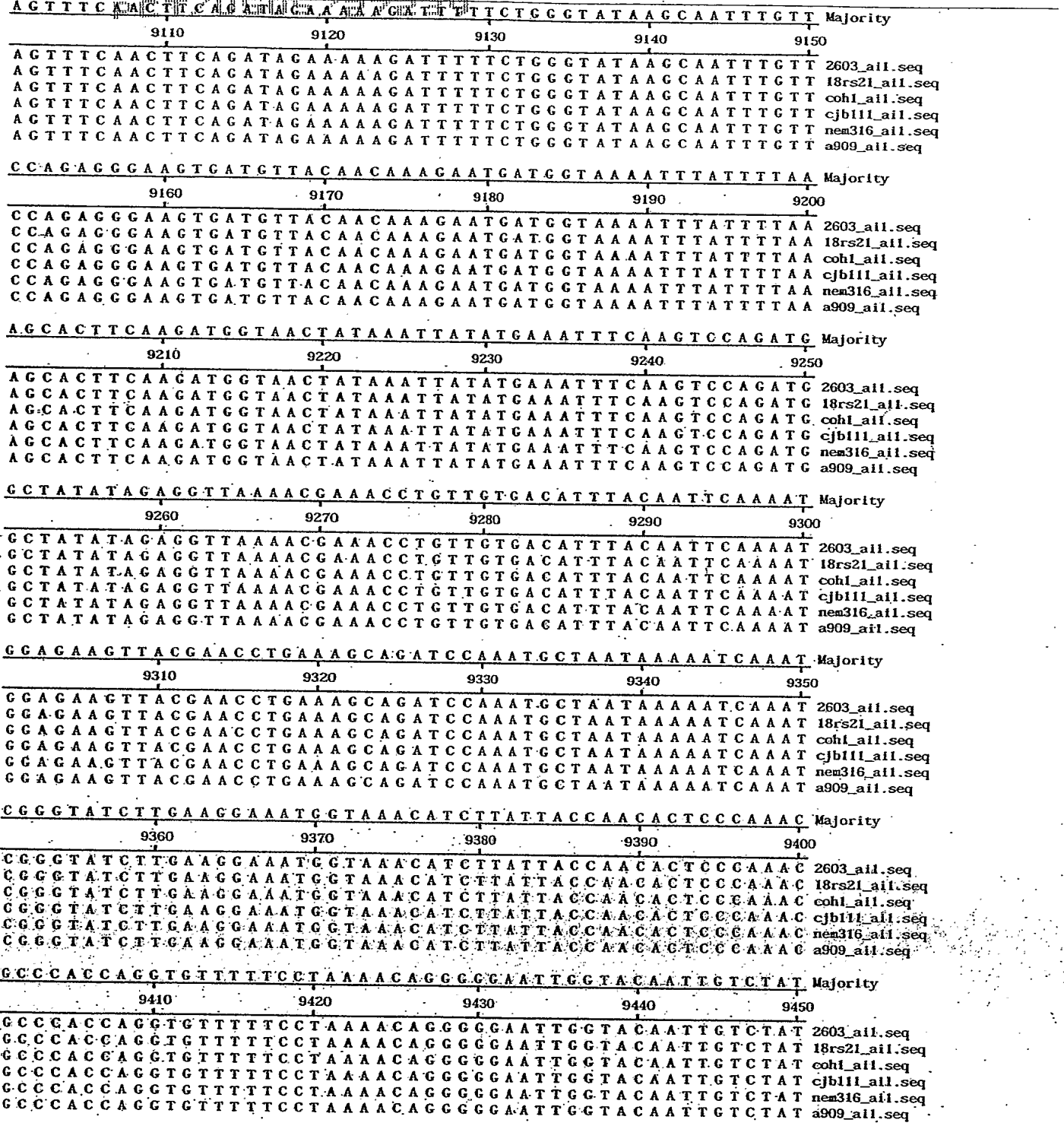
FIGURE 18 Y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9101 AGTTTCAACTTCAGATAGAAAAAGATTTTTCTGGGTATAAGCAATTTGTT nem316_all.seq
9100 AGTTTCAACTTCAGATAGAAAAAGATTTTTCTGGGTATAAGCAATTTGTT a909_all.seq
Majority
9160 9170 9180 9190 9200
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8917 CCAGAGGGAAGTGATGTTACAACAAAGAATGATGGTAAAATTTATTTTAA 18rs21_all.seq
9149 CCAGAGGGAAGTGATGTTACAACAAAGAATGATGGTAAAATTTATTTTAA cohl_all.seq
9149 CCAGAGGGAAGTGATGTTACAACAAAGAATGATGGTAAAATTTATTTTAA cjb111_all.seq
9151 CCAGAGGGAAGTGATGTTACAACAAAGAATGATGGTAAAATTTATTTTAA nem316_all.seq
9150 CCAGAGGGAAGTGATGTTACAACAAAGAATGATGGTAAAATTTATTTTAA a909_all.seq
Majority
9210 9220 9230 9240 9250
9194 AGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATG 2603_all.seq
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9199 AGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATG cjb111_all.seq
9201 AGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATG nem316_all.seq
9200 AGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATG a909_all.seq
Majority
9260 9270 9280 9290 9300
9244 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT 2603_all.seq
9017 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT 18rs21_all.seq
9249 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT cohl_all.seq
9249 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT cjb111_all.seq
9251 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT nem316_all.seq
9250 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCAAAAT a909_all.seq
Majority
9310 9320 9330 9340 9350
9294 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT 2603_all.seq
9067 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT 18rs21_all.seq
9299 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT cohl_all.seq
9299 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT cjb111_all.seq
9301 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT nem316_all.seq
9300 GGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAAAATCAAAT a909_all.seq
Majority
9360 9370 9380 9390 9400
9344 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC 2603_all.seq
9117 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC 18rs21_all.seq
9349 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC cohl_all.seq
9349 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC cjb111_all.seq
9351 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC nem316_all.seq
9350 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC a909_all.seq
Majority
9410 9420 9430 9440 9450
9394 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT 2603_all.seq
9167 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT 18rs21_all.seq
9399 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT cohl_all.seq
9399 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT cjb111_all.seq
9401 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT nem316_all.seq
9400 GCCCACCAGGTGTTTTTCCTAAAACAGGGGCGAATTGGTACAATTGTCTAT a909_all.seq

FIGURE 18 Z

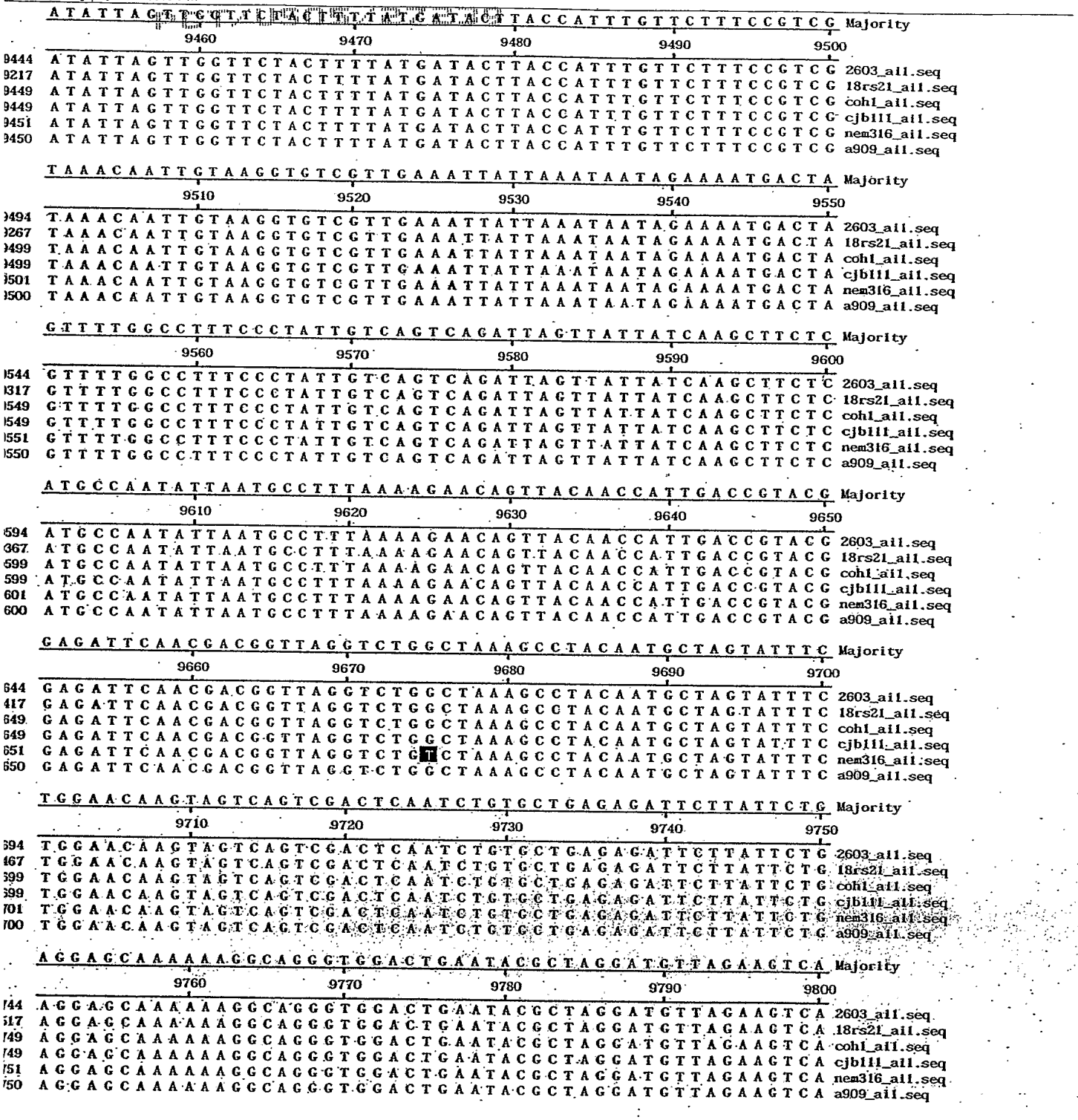
Majority
2603_all.seq
18rs21_all.seq
cohl_all.seq
cjblll_all.seq
nem316_all.seq
a909_all.seq

FIGURE 18 AA

```
      GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA Majority
               9810      9820      9830      9840      9850
794   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA 2603_ail.seq
567   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA 18rs21_ail.seq
799   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA coh1_ail.seq
799   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA cjb111_ail.seq
801   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA nem316_ail.seq
800   GAGAGCAGGTTGACCATGTGATGATTCCAAAAATCAATCAGGATTTACCA a909_ail.seq

      ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT Majority
               9860      9870      9880      9890      9900
844   ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT 2603_ail.seq
617   ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT 18rs21_ail.seq
849   ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT coh1_ail.seq
849   ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT cjb111_ail.seq
851   ATCTACGCTGGTCCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT nem316_ail.seq
850   ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT a909_ail.seq

      AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA Majority
               9910      9920      9930      9940      9950
894   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA 2603_ail.seq
667   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA 18rs21_ail.seq
899   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA coh1_ail.seq
899   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA cjb111_ail.seq
901   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA nem316_ail.seq
900   AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA a909_ail.seq

      GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG Majority
               9960      9970      9980      9990      10000
944   GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG 2603_ail.seq
717   GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG 18rs21_ail.seq
949   GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG coh1_ail.seq
949   GCGGTCAAAGAGGTATGTCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG cjb111_ail.seq
951   GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG nem316_ail.seq
950   GCGGTCAAAGAGGTATGTCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG a909_ail.seq

      ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC Majority
              10010     10020     10030     10040     10050
994   ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC 2603_ail.seq
767   ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC 18rs21_ail.seq
999   ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC coh1_ail.seq
999   ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC cjb111_ail.seq
0001  ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC nem316_ail.seq
0000  ATGAAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAAACCTTGGC a909_ail.seq

      TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG Majority
              10060     10070     10080     10090     10100
0044  TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG 2603_ail.seq
817   TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG 18rs21_ail.seq
0049  TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG coh1_ail.seq
0049  TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG cjb111_ail.seq
0051  TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG nem316_ail.seq
0050  TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG a909_ail.seq

      TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT Majority
              10110     10120     10130     10140     10150
0094  TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT 2603_ail.seq
867   TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT 18rs21_ail.seq
0099  TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT coh1_ail.seq
0099  TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT cjb111_ail.seq
0101  TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT nem316_ail.seq
0100  TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT a909_ail.seq
```

FIGURE 18 AB

```
      TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG Majority
               10160     10170     10180     10190     10200
10144 TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG 2603_all.seq
9917  TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG 18rs21_all.seq
10149 TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG coh1_all.seq
10149 TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG cjb111_all.seq
10151 TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG nem316_all.seq
10150 TATATGGGCTCTTTGTCAACTGTAATGGGTGACTTATCATTAACAACGAG a909_all.seq

      AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA Majority
               10210     10220     10230     10240     10250
10194 AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA 2603_all.seq
9967  AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA 18rs21_all.seq
10199 AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA coh1_all.seq
10199 AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA cjb111_all.seq
10201 AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA nem316_all.seq
10200 AGAGAATCAGCTTGGTTCTCTCTCTTTTTGGATGTTCAAAGCGATGAGAA a909_all.seq

      TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG Majority
               10260     10270     10280     10290     10300
10244 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG 2603_all.seq
10017 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG 18rs21_all.seq
10249 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG coh1_all.seq
10249 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG cjb111_all.seq
10251 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG nem316_all.seq
10250 TTTTGCTTTTTAAAATTTTTAAAGTTGCGAAAGCCAAAGGCTTGTCGCTTG a909_all.seq

      ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA Majority
               10310     10320     10330     10340     10350
10294 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA 2603_all.seq
10067 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA 18rs21_all.seq
10299 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA coh1_all.seq
10299 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA cjb111_all.seq
10301 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA nem316_all.seq
10300 ATGTCTTTGATAAGCTTGTTGGTCGCTTCTAATTTGGCATTGGAAAGGGA a909_all.seq

      TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA Majority
               10360     10370     10380     10390     10400
10344 TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA 2603_all.seq
10117 TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA 18rs21_all.seq
10349 TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA coh1_all.seq
10349 TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA cjb111_all.seq
0351  TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA nem316_all.seq
0350  TAGCTGAGGGCGTTTGTGATGTAAGTTTTGTACTTCATGAAGGTCCTAAA a909_all.seq

      GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC Majority
               10410     10420     10430     10440     10450
0394  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC 2603_all.seq
0167  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC 18rs21_all.seq
0399  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC coh1_all.seq
0399  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC cjb111_all.seq
0401  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC nem316_all.seq
0400  GACCATTTTAAAAGCAGAATTGCCAGTTGTTACGTTATCATCTATGAAGC a909_all.seq

      TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA Majority
               10460     10470     10480     10490     10500
0444  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA 2603_all.seq
0217  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA 18rs21_all.seq
0449  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA coh1_all.seq
0449  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA cjb111_all.seq
0451  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA nem316_all.seq
0450  TAAAGAATTCAGTTGTTCGCTTTTCTTAGAAATGAAAGAGTATGAGCTGA a909_all.seq
```

FIGURE 18 AC

```
      TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA Majority
                10510       10520       10530       10540       10550
10494 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA 2603_all.seq
10267 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA 18rs21_all.seq
10499 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA cohl_all.seq
10499 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA cjb111_all.seq
10501 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA nem316_all.seq
10500 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA a909_all.seq

      AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC Majority
                10560       10570       10580       10590       10600
10544 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC 2603_all.seq
10317 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC 18rs21_all.seq
10549 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC cohl_all.seq
10549 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC cjb111_all.seq
10551 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC nem316_all.seq
10550 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC a909_all.seq

      TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA Majority
                10610       10620       10630       10640       10650
10594 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA 2603_all.seq
10367 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA 18rs21_all.seq
10599 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA cohl_all.seq
10599 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA cjb111_all.seq
10601 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA nem316_all.seq
10600 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA a909_all.seq

      AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA Majority
                10660       10670       10680       10690       10700
10644 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA 2603_all.seq
10417 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA 18rs21_all.seq
10649 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA cohl_all.seq
10649 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA cjb111_all.seq
10651 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA nem316_all.seq
10650 AAAGTTCTATCATCCTCTTTTGGCGCCTTTTTTCCAGCAGATAATATTAA a909_all.seq

      GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG Majority
                10710       10720       10730       10740       10750
0694 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG 2603_all.seq
0467 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG 18rs21_all.seq
0699 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG cohl_all.seq
0699 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG cjb111_all.seq
0701 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG nem316_all.seq
0700 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG a909_all.seq

      CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA Majority
                10760       10770       10780       10790       10800
0744 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA 2603_all.seq
0517 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA 18rs21_all.seq
0749 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA cohl_all.seq
0749 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA cjb111_all.seq
0751 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA nem316_all.seq
0750 CAAACTACACCACTCAGATTCAAGCTATTGGGACAACGATTAAGTCACAA a909_all.seq

      ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG Majority
                10810       10820       10830       10840       10850
0794 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG 2603_all.seq
0567 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG 18rs21_all.seq
0799 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG cohl_all.seq
0799 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG cjb111_all.seq
0801 ATTCCGGAATCGATTTTGACGATTACGGATAAAAAGAGCAGGAAGTTCAG nem316_all.seq
0800 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG a909_all.seq
```

FIGURE 18 AD

```
                CATTAACAACATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA Majority
                        10860     10870     10880     10890     10900
10844 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA
10617 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA 2603_all.seq
10849 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA 18rs21_all.seq
10849 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA cohl_all.seq
10851 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA cjb111_all.seq
10850 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA nem316_all.seq
                CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA a909_all.seq

                CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT Majority
                        10910     10920     10930     10940     10950
10894 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT
10667 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT 2603_all.seq
10899 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT 18rs21_all.seq
10899 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT cohl_all.seq
10901 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT cjb111_all.seq
10900 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT nem316_all.seq
                CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT a909_all.seq

                TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT Majority
                        10960     10970     10980     10990     11000
10944 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT
10717 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT 2603_all.seq
10949 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT 18rs21_all.seq
10949 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT cohl_all.seq
10951 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACTCTTACCTT cjb111_all.seq
10950 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT nem316_all.seq
                TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACTCTTACCTT a909_all.seq

                TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA Majority
                        11010     11020     11030     11040     11050
10994 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA
10767 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA 2603_all.seq
10999 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA 18rs21_all.seq
10999 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA cohl_all.seq
11001 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA cjb111_all.seq
11000 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA nem316_all.seq
                TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA a909_all.seq

                ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA Majority
                        11060     11070     11080     11090     11100
11044 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA
10817 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA 2603_all.seq
11049 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA 18rs21_all.seq
11049 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA cohl_all.seq
11051 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA cjb111_all.seq
11050 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA nem316_all.seq
                ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA a909_all.seq

                GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC Majority
                        11110     11120     11130     11140     11150
11094 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC
10867 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC 2603_all.seq
11099 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC 18rs21_all.seq
11099 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC cohl_all.seq
11101 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC cjb111_all.seq
11100 GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC nem316_all.seq
                GGAAAAACGACAATTGTGGATGAAGCTAACTTCAAAGAGGCTGATTACCC a909_all.seq

                AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA Majority
                        11160     11170     11180     11190     11200
11144 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA
10917 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA 2603_all.seq
11149 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA 18rs21_all.seq
11149 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA cohl_all.seq
11151 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA cjb111_all.seq
11150 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA nem316_all.seq
                AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA a909_all.seq
```

FIGURE 18 AE

```
      GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  Majority
               11210     11220     11230     11240     11250
11194 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  2603_ai1.seq
10967 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  18rs21_ai1.seq
11199 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  coh1_ai1.seq
11199 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  cjb111_ai1.seq
11201 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  nem316_ai1.seq
11200 GCAAAGGGTAAAAATCCTTTATTTTAAGCACTTTTTCAAGCATTTTGTCT  a909_ai1.seq

      TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  Majority
               11260     11270     11280     11290     11300
11244 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  2603_ai1.seq
11017 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  18rs21_ai1.seq
11249 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  coh1_ai1.seq
11249 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  cjb111_ai1.seq
11251 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  nem316_ai1.seq
11250 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG  a909_ai1.seq

      ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  Majority
               11310     11320     11330     11340     11350
11294 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  2603_ai1.seq
11067 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  18rs21_ai1.seq
11299 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  coh1_ai1.seq
11299 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  cjb111_ai1.seq
11301 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  nem316_ai1.seq
11300 ACGTGACCGTTTGTTTTGAAGTGGCTTGCGTAGACAAAAAAATAGATACG  a909_ai1.seq

      TCAGATAAATTTCTGGCATTACGAGAACATTTTTAGAGTGTTCTCTTTTT  Majority
               11360     11370     11380     11390     11400
11344 TCAGATAAATTTCTGGCATTACGAGAACATTTTTAGAGTGTTCTCTTTTT  2603_ai1.seq
11117 TCAGATAAATTTCTGGCATTACGAGAACATTTTTAGAGTGTTCTCTTTTT  18rs21_ai1.seq
11349 TCAGATAAATTTCTGGCATTACGAGAACATTTTTAGAGTGTTCTCTTTTT  coh1_ai1.seq
11349 TCAGATAAATTTCTGGCATTACGAGAACATTTCTAGAGTGTTCTCTTTTT  cjb111_ai1.seq
11351 TCAGATAAATTTCTGGCATTACGAGAACATTTTTAGAGTGTTCTCTTTTT  nem316_ai1.seq
11350 TCAGATAAATTTCTGGCATTACGAGAACATTTCTAGAGTGTTCTCTTTTT  a909_ai1.seq

      TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  Majority
               11410     11420     11430     11440     11450
1394  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  2603_ai1.seq
1167  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  18rs21_ai1.seq
1399  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  coh1_ai1.seq
1399  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  cjb111_ai1.seq
1401  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  nem316_ai1.seq
1400  TTAGTTTACGGAGGAAAAATATATATGGAAAAACAGGATTCACGAGTTCT  a909_ai1.seq

      CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  Majority
               11460     11470     11480     11490     11500
1444  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  2603_ai1.seq
1217  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  18rs21_ai1.seq
1449  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  coh1_ai1.seq
1449  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  cjb111_ai1.seq
1451  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  nem316_ai1.seq
1450  CATCCATTGGGAGGGGAATTCTGGGGACAAGCTCATTGAACACCAAACCA  a909_ai1.seq

      GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  Majority
               11510     11520     11530     11540     11550
1494  GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  2603_ai1.seq
1267  GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  18rs21_ai1.seq
1499  GCGCAATGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  coh1_ai1.seq
1499  GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  cjb111_ai1.seq
1501  GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  nem316_ai1.seq
1500  GCGCAACGGGGTGGTACTACCAAGTCGATCGTAGCTTTAGTCAACCAAAA  a909_ai1.seq
```

FIGURE 18 AF

```
      GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT Majority
               11560     11570     11580     11590     11600
11544 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT 2603_all.seq
11317 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT 18rs21_all.seq
11549 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT coh1_all.seq
11549 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT cjb111_all.seq
11551 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT nem316_all.seq
11550 GGGGAACCGCCCAGAATGATCCAAAGGCACTAGAAAGTGTCCGTAATGAT a909_all.seq

      TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC Majority
               11610     11620     11630     11640     11650
11594 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC 2603_all.seq
11367 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC 18rs21_all.seq
11599 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC coh1_all.seq
11599 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC cjb111_all.seq
11601 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC nem316_all.seq
11600 TCGATTTCGGGCGGTGATGATGTCATGGGTTATGCTTATAGCAAATGTAC a909_all.seq

      TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG Majority
               11660     11670     11680     11690     11700
1644  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG 2603_all.seq
1417  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG 18rs21_all.seq
1649  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG coh1_all.seq
1649  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG cjb111_all.seq
1651  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG nem316_all.seq
1650  TTGGGGAGTTGCGGCACGAATTAATCAGTGGGACTGAAACTCAAAGGTTG a909_all.seq

      AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT Majority
               11710     11720     11730     11740     11750
1694  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT 2603_all.seq
1467  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT 18rs21_all.seq
1699  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT coh1_all.seq
1699  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT cjb111_all.seq
1701  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT nem316_all.seq
1700  AAATGGTGAGAAGATTACCATTACCAGTTCAATGGGAAATGGTCAGGATT a909_all.seq

      GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA Majority
               11760     11770     11780     11790     11800
1744  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA 2603_all.seq
1517  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA 18rs21_all.seq
1749  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA coh1_all.seq
1749  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA cjb111_all.seq
1751  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA nem316_all.seq
1750  GGGTTGGAACAGCCGAAAGACTAGATGGTGAAACTGATACAGTTCCAAAA a909_all.seq

      GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG Majority
               11810     11820     11830     11840     11850
794   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG 2603_all.seq
567   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG 18rs21_all.seq
799   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG coh1_all.seq
799   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG cjb111_all.seq
801   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG nem316_all.seq
800   GAAGGTACTATTCTCTCTTTTTAGGAAAGTAGTTATGGTTCGTATATAGG a909_all.seq

      CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA Majority
               11860     11870     11880     11890     11900
844   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA 2603_all.seq
617   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA 18rs21_all.seq
849   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA coh1_all.seq
849   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA cjb111_all.seq
851   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA nem316_all.seq
850   CTACGGAACTATATCTTTCGTCACATTACATCTACAGATAGTACCATGAA a909_all.seq
```

FIGURE 18 AG

```
      TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT Majority

                11910       11920       11930       11940       11950
11894 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT 2603_all.seq
11667 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT 18rs21_all.seq
11899 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT cohl_all.seq
11899 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT cjb111_all.seq
11901 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT nem316_all.seq
11900 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT a909_all.seq

      TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT Majority

                11960       11970       11980       11990       12000
11944 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT 2603_all.seq
11717 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT 18rs21_all.seq
11949 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT cohl_all.seq
11949 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT cjb111_all.seq
11951 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT nem316_all.seq
11950 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT a909_all.seq

      GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT Majority

                12010       12020       12030       12040       12050
11994 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT 2603_all.seq
11767 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT 18rs21_all.seq
11999 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT cohl_all.seq
11999 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT cjb111_all.seq
12001 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT nem316_all.seq
12000 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT a909_all.seq

      AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG Majority

                12060       12070       12080       12090       12100
12044 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG 2603_all.seq
11817 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG 18rs21_all.seq
12049 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG cohl_all.seq
12049 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG cjb111_all.seq
12051 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG nem316_all.seq
12050 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG a909_all.seq

      CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC Majority

                12110       12120       12130       12140       12150
2094  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC 2603_all.seq
1867  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC 18rs21_all.seq
2099  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC cohl_all.seq
2099  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC cjb111_all.seq
2101  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC nem316_all.seq
2100  CTAATAGTTCTAGAACTTCTAATTGTTTTTTCGTCGACGATATGAATTTTC a909_all.seq

      AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA Majority

                12160       12170       12180       12190       12200
2144  AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA 2603_all.seq
1917  AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA 18rs21_all.seq
2149  AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA cohl_all.seq
2149  AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA cjb111_all.seq
2151  AATCTTAACTGTTAGAATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA nem316_all.seq
2150  AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAAGGTCA a909_all.seq

      GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT Majority

                12210       12220       12230       12240       12250
2194  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT 2603_all.seq
1967  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT 18rs21_all.seq
2199  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT cohl_all.seq
2199  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT cjb111_all.seq
2201  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT nem316_all.seq
2200  GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT a909_all.seq
```

FIGURE 18 AH

```
      TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG Majority
               12260     12270     12280     12290     12300
12244 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG 2603_ail.seq
12017 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG 18rs21_ail.seq
12249 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG cohl_ail.seq
12249 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG cjb111_ail.seq
12251 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG nem316_ail.seq
12250 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG a909_ail.seq

      AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT Majority
               12310     12320     12330     12340     12350
12294 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT 2603_ail.seq
12067 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT 18rs21_ail.seq
12299 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT cohl_ail.seq
12299 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT cjb111_ail.seq
12301 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT nem316_ail.seq
12300 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAAATGCT a909_ail.seq

      CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA Majority
               12360     12370     12380     12390     12400
2344  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA 2603_ail.seq
2117  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA 18rs21_ail.seq
2349  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA cohl_ail.seq
2349  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA cjb111_ail.seq
2351  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA nem316_ail.seq
2350  CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA a909_ail.seq

      ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT Majority
               12410     12420     12430     12440     12450
2394  ACTTGATAATCGGTTGTCTCCGACTGAAAAAAAGTTATTGATTACCTTAT 2603_ail.seq
2167  ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT 18rs21_ail.seq
2399  ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT cohl_ail.seq
2399  ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT cjb111_ail.seq
2401  ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT nem316_ail.seq
2400  ACTTGATAATCGGTTGTCTCCGACTGAACAAAAGTTATTGATTACCTTAT a909_ail.seq

      TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA Majority
               12460     12470     12480     12490     12500
2444  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA 2603_ail.seq
2217  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA 18rs21_ail.seq
2449  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA cohl_ail.seq
2449  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA cjb111_ail.seq
2451  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA nem316_ail.seq
2450  TATTACATACTAAAGGTTTAATCATTGATATGTAAGAAGTAAGTCAGCTA a909_ail.seq

      ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG Majority
               12510     12520     12530     12540     12550
2494  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG 2603_ail.seq
2267  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG 18rs21_ail.seq
2499  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG cohl_ail.seq
2499  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG cjb111_ail.seq
2501  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG nem316_ail.seq
2500  ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG a909_ail.seq

      AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA Majority
               12560     12570     12580     12590     12600
2544  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA 2603_ail.seq
2317  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA 18rs21_ail.seq
2549  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA cohl_ail.seq
2549  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA cjb111_ail.seq
2551  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA nem316_ail.seq
2550  AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA a909_ail.seq
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FIGURE 18 AI

```
     AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG Majority
              12610     12620     12630     12640     12650
2594 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG 2603_all.seq
2367 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG 18rs21_all.seq
2599 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG cohl_all.seq
2599 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG cjb111_all.seq
2601 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG nem316_all.seq
2600 AAAAATATGATATTTGAAGAGTCCAAAGATCTAATAGATAGTCCAGTTAG a909_all.seq

     AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC Majority
              12660     12670     12680     12690     12700
2644 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC 2603_all.seq
2417 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC 18rs21_all.seq
2649 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC cohl_all.seq
2649 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC cjb111_all.seq
2651 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC nem316_all.seq
2650 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC a909_all.seq

     TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT Majority
              12710     12720     12730     12740     12750
2694 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT 2603_all.seq
2467 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT 18rs21_all.seq
2699 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT cohl_all.seq
2699 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT cjb111_all.seq
2701 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT nem316_all.seq
2700 TATTATTTTAACCGACTTATTTTAAAGACTTATCATATCTAGGCTTGCTT a909_all.seq

     GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA Majority
              12760     12770     12780     12790     12800
2744 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA 2603_all.seq
2517 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA 18rs21_all.seq
2749 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA cohl_all.seq
2749 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA cjb111_all.seq
2751 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA nem316_all.seq
2750 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA a909_all.seq

     AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG Majority
              12810     12820     12830     12840     12850
2794 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG 2603_all.seq
2567 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG 18rs21_all.seq
2799 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG cohl_all.seq
2799 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG cjb111_all.seq
2801 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG nem316_all.seq
2800 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG a909_all.seq

     AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC Majority
              12860     12870     12880     12890     12900
2844 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC 2603_all.seq
2617 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC 18rs21_all.seq
2849 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC cohl_all.seq
2849 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC cjb111_all.seq
2851 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC nem316_all.seq
2850 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAAATAGC a909_all.seq

     TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA Majority
              12910     12920     12930     12940     12950
2894 TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA 2603_all.seq
2667 TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA 18rs21_all.seq
2899 TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA cohl_all.seq
2899 TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA cjb111_all.seq
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2900 TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTTAACA a909_all.seq
```

FIGURE 18 AJ

```
      C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  Majority
                     12960         12970         12980         12990         13000
12944 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  2603_all.seq
12717 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  18rs21_all.seq
12949 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  coh1_all.seq
12949 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  cjb111_all.seq
12951 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A -  nem316_all.seq
12950 C T A A G A A T G A T G A A G A C C C T C G T A T T G A A G A A G A A G T T G A G C A G C T A G A A  a909_all.seq

      G A T A A G A T                                                                              Majority

12994 G A T A A G A T                                                                              2603_all.seq
12767 G A T A A G A T                                                                              18rs21_all.seq
12999 G A T A A G A T                                                                              coh1_all.seq
12999 G A                                                                                          cjb111_all.seq
13000 - A                                                                                          nem316_all.seq
13000 G A T A A G A T                                                                              a909_all.seq
```

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 18 AK

```
    GGCCTTGTTCCGATGTTGATCCCGATAACTCCTGGCTCATTAATAGCCTG Majority
             10        20        30        40        50
1   GGCCTTGTTCCGATGTTGATTCCGATAACTCCTGGCTCATTAATAGCCTG 2603_ai2.seq
1   GGCCTTGTTCCGATGTTGATTCCGATAACTCCTGGCTCATTAATAGCCTG 18rs21_ai2.seq
1   GGCCTTGTTCCGATGTTGATCCCGATAACTCCTGGCTCATTAATAGCCTG 515_ai2.seq
1   GGCCTTGTTCCGATGTTGATCCCGATAACTCCTGGCTCATTAATAGCCTG cjb111_ai2.seq
1   GGCCTTGTTCCGATGTTGATCCCGATAACTCCTGGCTCATTAATAGCCTG h36b_ai2.seq

    TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT Majority
             60        70        80        90        100
51  TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT 2603_ai2.seq
51  TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT 18rs21_ai2.seq
51  TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT 515_ai2.seq
51  TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT cjb111_ai2.seq
51  TTCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAAT h36b_ai2.seq

    TTTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATG Majority
             110       120       130       140       150
101 TTTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATG 2603_ai2.seq
101 TTTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATG 18rs21_ai2.seq
101 TTTGAAAATAGACTAAGTATTTATTAACTTCAGGCCACTTTCTATGCATG 515_ai2.seq
101 TTTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATG cjb111_ai2.seq
101 TTTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATG h36b_ai2.seq

    AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC Majority
             160       170       180       190       200
151 AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC 2603_ai2.seq
151 AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC 18rs21_ai2.seq
151 AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC 515_ai2.seq
151 AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC cjb111_ai2.seq
151 AAATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAAC h36b_ai2.seq

    TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG Majority
             210       220       230       240       250
201 TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG 2603_ai2.seq
201 TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG 18rs21_ai2.seq
201 TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG 515_ai2.seq
201 TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG cjb111_ai2.seq
201 TATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCCTCCTCTAG h36b_ai2.seq

    CAACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT Majority
             260       270       280       290       300
251 CAACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT 2603_ai2.seq
251 CAACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT 18rs21_ai2.seq
251 CAACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT 515_ai2.seq
251 CAACTGTTCCATCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT cjb111_ai2.seq
251 CAACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAAT h36b_ai2.seq

    TTAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACG Majority
             310       320       330       340       350
301 TTAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACG 2603_ai2.seq
301 TTAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACG 18rs21_ai2.seq
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301 TTAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACG cjb111_ai2.seq
301 TTAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACG h36b_ai2.seq

    ATAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACC Majority
             360       370       380       390       400
351 ATAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACC 2603_ai2.seq
351 ATAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACC 18rs21_ai2.seq
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351 ATAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACC cjb111_ai2.seq
351 ATAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACC h36b_ai2.seq

    TCACTACTACAATAAAACTAAAAAAGATTGGAACGTCAGTTAGTCCCAAT Majority
             410       420       430       440       450
401 TCACTACTACAATAAAACTAAAAAAGATTGGAACGTCAGTTAGTCCCAAT 2603_ai2.seq
401 TCACTACTACAATAAAACTAAAAAAGATTGGAACGTCAGTTAGTCCCAAT 18rs21_ai2.seq
401 TCACTACTACAATAAAACTAAAAAAGATTGGAACATCAGTTAGTCCCAAT 515_ai2.seq
401 TCACTACTACAATAAAACTAAAAAAGATTGGAACTAACTGACGTTCCAAT cjb111_ai2.seq
401 TCACTACTACAATAAAACTAAAAAAGATTGGAACGTCAGTTAGTCCCAAT h36b_ai2.seq
```

Figure 19

```
     CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC Majority
              460       470       480       490       500
451  CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC 2603_a12.seq
451  CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC 18rs21_a12.seq
451  CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC 515_a12.seq
451  CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC cjb111_a12.seq
451  CTTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATAC h36b_a12.seq

     GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC Majority
              510       520       530       540       550
501  GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC 2603_a12.seq
501  GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC 18rs21_a12.seq
501  GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC 515_a12.seq
501  GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC cjb111_a12.seq
501  GCAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATC h36b_a12.seq

     TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA Majority
              560       570       580       590       600
551  TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA 2603_a12.seq
551  TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA 18rs21_a12.seq
551  TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA 515_a12.seq
551  TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA cjb111_a12.seq
551  TGTCGGAAAATGAACCCCTAGGTAAATACGAGATAACCCAATTAAAAAAA h36b_a12.seq

     TGAGCAAACCCAAAGTACCTTGGCACAACAGTTTCCATATACTCTTAGGC Majority
              610       620       630       640       650
601  TGAGCAAACCCAAAGTACCTTGGCACAACAGTTTCCATATACTCTTAGGC 2603_a12.seq
601  TGAGCAAACCCAAAGTACCTTGGCACAACAGTTTCCATATACTCTTAGGC 18rs21_a12.seq
601  TGAGCAAACCCAAAATACCTTGGCACAACAGTTTCCATATACTCTTAGGC 515_a12.seq
601  TGAGCAAACCCAAAATACCTTGGTACAACAGTTTCCATATACTATTAGGC cjb111_a12.seq
601  TGAGCAAACCCAAAGTACCTTGGCACAACAGTTTCCATATACTCTTAGGC h36b_a12.seq

     ATATAGTACTGCAATAAAATAATAATACTCCCAAATATCATAAATGTTCC Majority
              660       670       680       690       700
651  ATATAGTACTGCAATAAAATAATAATACTCCCAAATATCATAAATGTTCC 2603_a12.seq
651  ATATAGTACTGCAATAAAATAATAATACTCCCAAATATCATAAATGTTCC 18rs21_a12.seq
651  ATATAGTACTGCAATAAAATAATAATACTCCCAAATATCATAAATGTTCC 515_a12.seq
651  ATATAGTACTGCAATAAGATAATAATACTCCCAAATATCATAAATGTTCC cjb111_a12.seq
651  ATATAGTACTGCAATAAAATAATAATACTCCCAAATATCATAAATGTTCC h36b_a12.seq

     CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG Majority
              710       720       730       740       750
701  CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG 2603_a12.seq
701  CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG 18rs21_a12.seq
701  CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG 515_a12.seq
701  CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG cjb111_a12.seq
701  CATCGAGTGCCCACTGGGAAACGAATAGCCACCTGCAAATACTAAATGGG h36b_a12.seq

     TTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT Majority
              760       770       780       790       800
751  TTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT 2603_a12.seq
751  TTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT 18rs21_a12.seq
751  GTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT 515_a12.seq
751  TTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT cjb111_a12.seq
751  TTAAAGTTGGTCTTACTCTTTGAAAAATAAGTTTTAAAGAAAGTATACAT h36b_a12.seq

     ATACCAGAGATAATAGCATTTACTGCGATAAATCTAGCTTGAGGATACCA Majority
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801  ATACCAGAGATAATAGCATTTACTGCGATAAATCTAGCTTGAGGATACCA 2603_a12.seq
801  ATACCAGAGATAATAGCATTTACTGCGATAAATCTAGCTTGAGGATACCA 18rs21_a12.seq
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     CTTCTTAAGGTAACAGAAAGTGACGCTCATAATCGCAATAGCTATCTGGC Majority
              860       870       880       890       900
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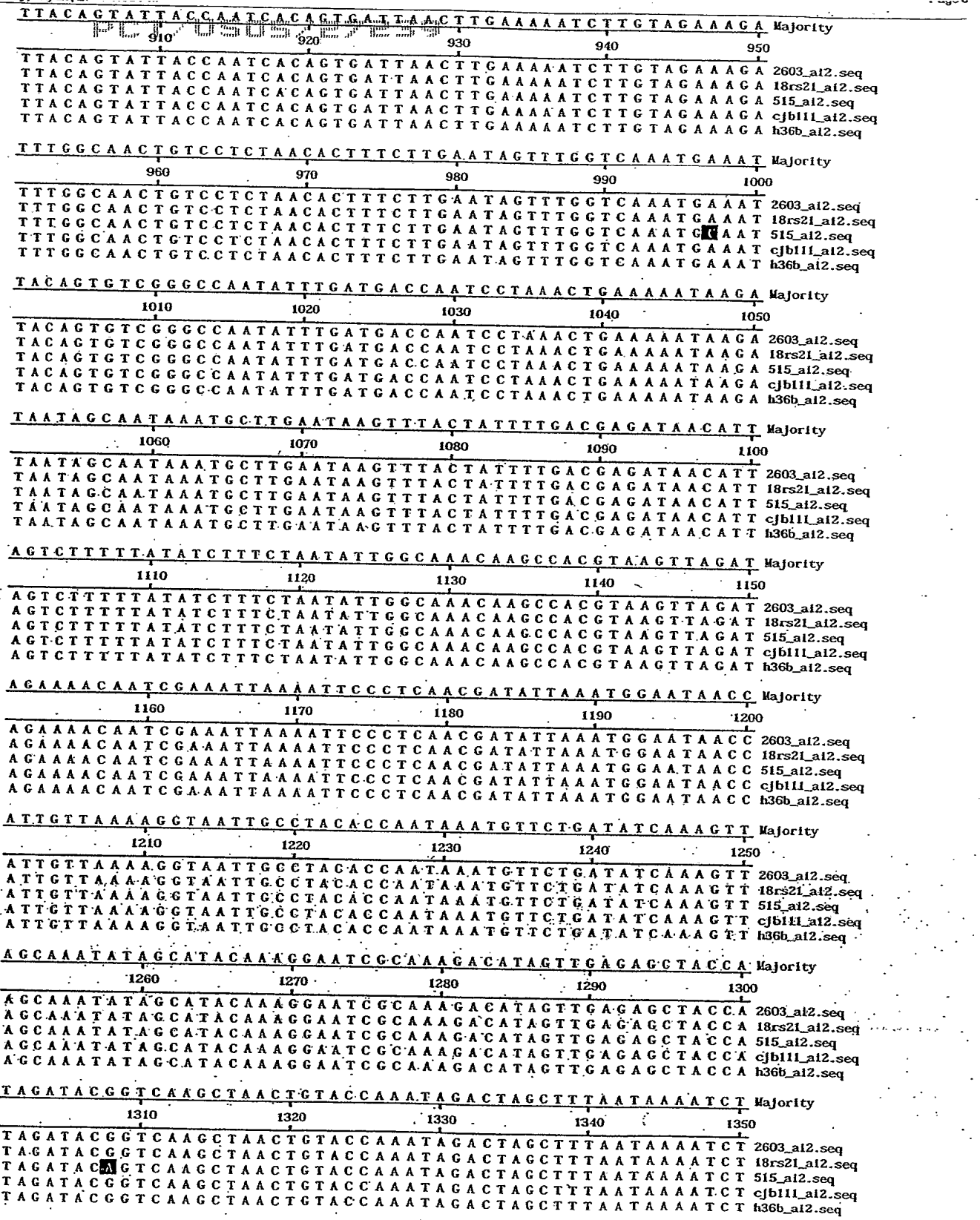
```

FIGURE 19A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901 TTACAGTATTACCAATCACAGTGATTAACTTGAAAAATCTTGTAGAAAGA 18rs21_al2.seq
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960 970 980 990 1000
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951 TTTGGCAACTGTCCTCTAACACTTTCTTGAATAGTTTGGTCAAATGAAAT h36b_al2.seq
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1010 1020 1030 1040 1050
1001 TACAGTGTCGGGCCAATATTTGATGACCAATCCTAAACTGAAAAATAAGA 2603_al2.seq
1001 TACAGTGTCGGGCCAATATTTGATGACCAATCCTAAACTGAAAAATAAGA 18rs21_al2.seq
1001 TACAGTGTCGGGCCAATATTTGATGACCAATCCTAAACTGAAAAATAAGA 515_al2.seq
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1060 1070 1080 1090 1100
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1110 1120 1130 1140 1150
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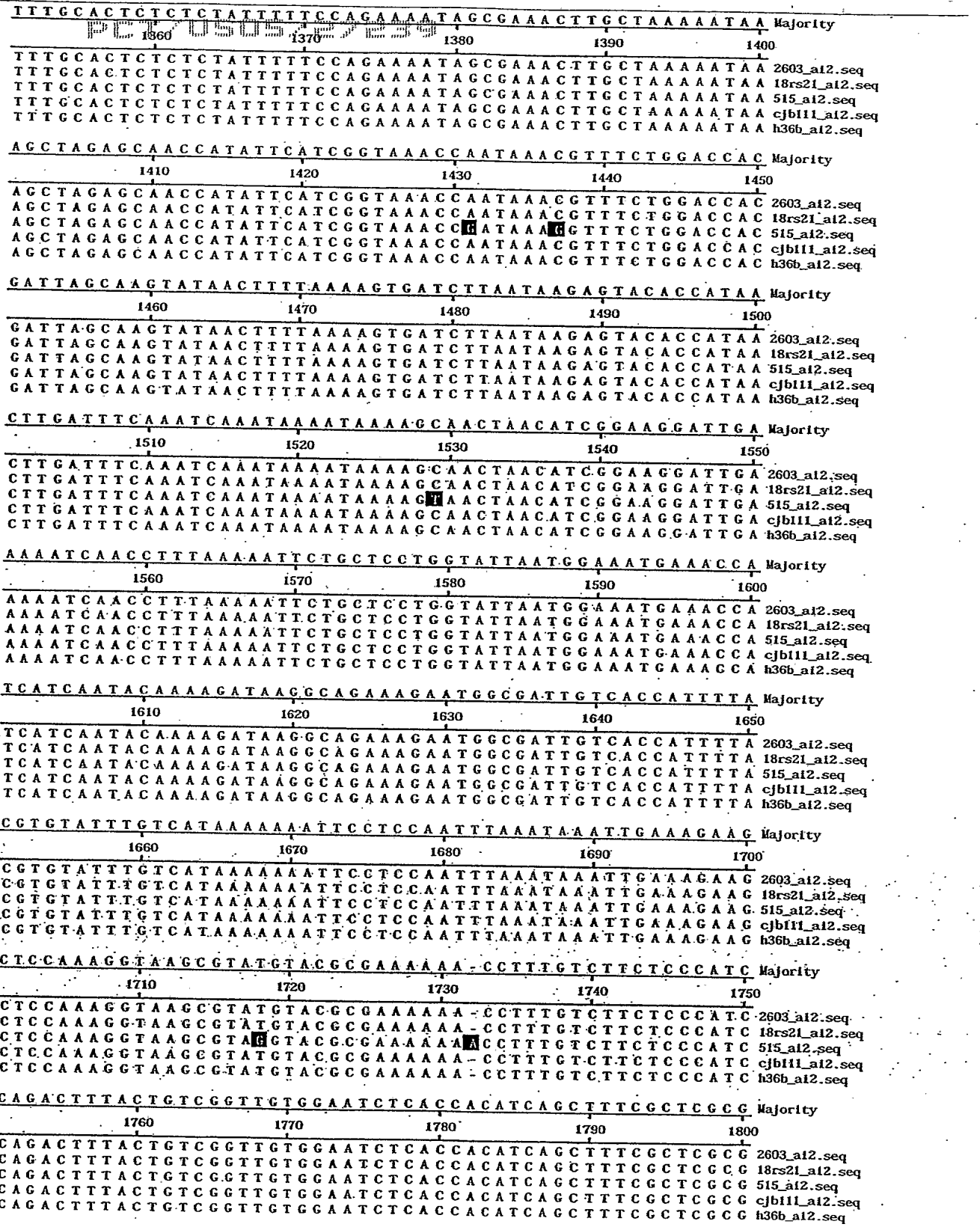
FIGURE 19B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AGCTAGAGCAACCATATTCATCGGTAAACCAATAAACGTTTCTGGACCAC Majority
1410 1420 1430 1440 1450
1401 AGCTAGAGCAACCATATTCATCGGTAAACCAATAAACGTTTCTGGACCAC 2603_a12.seq
1401 AGCTAGAGCAACCATATTCATCGGTAAACCAATAAACGTTTCTGGACCAC 18rs21_a12.seq
1401 AGCTAGAGCAACCATATTCATCGGTAAACCGATAAAGGTTTCTGGACCAC 515_a12.seq
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1460 1470 1480 1490 1500
1451 GATTAGCAAGTATAACTTTTAAAAGTGATCTTAATAAGAGTACACCATAA 2603_a12.seq
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1551 AAAATCAACCTTTAAAAATTCTGCTCCTGGTATTAATGGAAATGAAACCA 2603_a12.seq
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1651 CGTGTATTTGTCATAAAAAAAATTCCTCCAATTTAAATAAATTGAAAGAAG cjb111_a12.seq
1651 CGTGTATTTGTCATAAAAAAAATTCCTCCAATTTAAATAAATTGAAAGAAG h36b_a12.seq
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1701 CTCCAAAGGTAAGCGTATGTACGCGAAAAAAA-CCTTTGTCTTCTCCCATC 18rs21_a12.seq
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1701 CTCCAAAGGTAAGCGTATGTACGCGAAAAAAA-CCTTTGTCTTCTCCCATC cjb111_a12.seq
1701 CTCCAAAGGTAAGCGTATGTACGCGAAAAAAA-CCTTTGTCTTCTCCCATC h36b_a12.seq
CAGACTTTACTGTCGGTTGTGGAATCTCACCACATCAGCTTTCGCTCGCG Majority
1760 1770 1780 1790 1800
1750 CAGACTTTACTGTCGGTTGTGGAATCTCACCACATCAGCTTTCGCTCGCG 2603_a12.seq
1750 CAGACTTTACTGTCGGTTGTGGAATCTCACCACATCAGCTTTCGCTCGCG 18rs21_a12.seq
1751 CAGACTTTACTGTCGGTTGTGGAATCTCACCACATCAGCTTTCGCTCGCG 515_a12.seq
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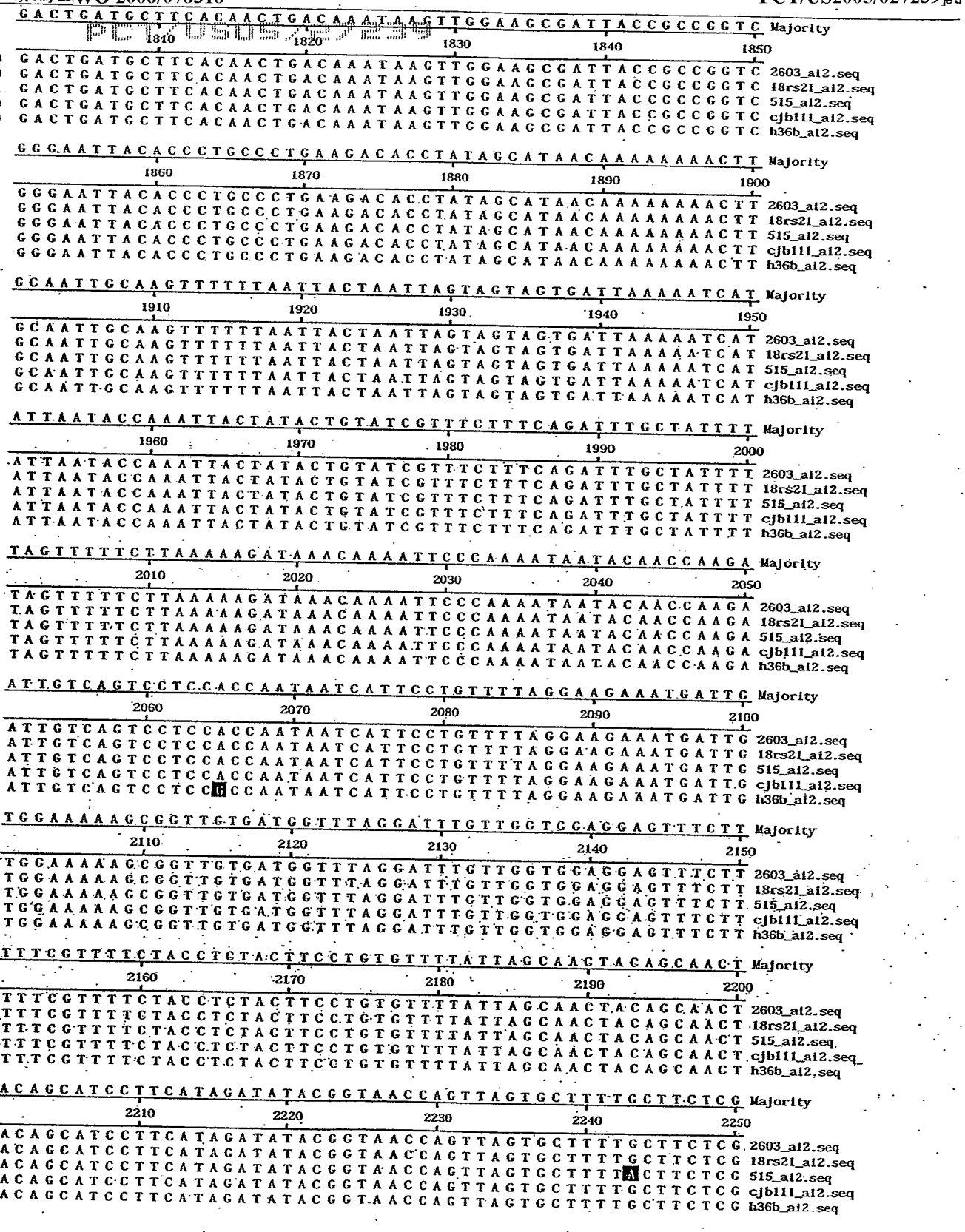
FIGURE 19C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1860 1870 1880 1890 1900
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1900 GCAATTGCAAGTTTTTTAATTACTAATTAGTAGTAGTGATTAAAAATCAT h36b_al2.seq
ATTAATACCAAATTACTATACTGTATCGTTTCTTTCAGATTTGCTATTTT Majority
1960 1970 1980 1990 2000
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1950 ATTAATACCAAATTACTATACTGTATCGTTTCTTTCAGATTTGCTATTTT 18rs21_al2.seq
1951 ATTAATACCAAATTACTATACTGTATCGTTTCTTTCAGATTTGCTATTTT 515_al2.seq
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1950 ATTAATACCAAATTACTATACTGTATCGTTTCTTTCAGATTTGCTATTTT h36b_al2.seq
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2000 TAGTTTTTCTTAAAAAGATAAACAAAATTCCCAAAATAATACAACCAAGA 2603_al2.seq
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2000 TAGTTTTTCTTAAAAAGATAAACAAAATTCCCAAAATAATACAACCAAGA cjb111_al2.seq
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2051 ATTGTCAGTCCTCCACCAATAATCATTCCTGTTTTAGGAAGAAATGATTG 515_al2.seq
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2110 2120 2130 2140 2150
2100 TGGAAAAAGCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTT 2603_al2.seq
2100 TGGAAAAAGCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTT 18rs21_al2.seq
2101 TGGAAAAAGCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTT 515_al2.seq
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2100 TGGAAAAAGCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTT h36b_al2.seq
TTTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACT Majority
2160 2170 2180 2190 2200
2150 TTTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACT 2603_al2.seq
2150 TTTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACT 18rs21_al2.seq
2151 TTTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACT 515_al2.seq
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2210 2220 2230 2240 2250
2200 ACAGCATCCTTCATAGATATACGGTAACCAGTTAGTGCTTTTGCTTCTCG 2603_al2.seq
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2200 ACAGCATCCTTCATAGATATACGGTAACCAGTTAGTGCTTTTGCTTCTCG h36b_al2.seq

FIGURE 19D

```
      AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT Majority
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2250  AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT 2603_al2.seq
2250  AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT 18rs21_al2.seq
2251  AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT 515_al2.seq
2250  AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT cjb111_al2.seq
2250  AAAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTAT h36b_al2.seq

      CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA Majority
               2310      2320      2330      2340      2350
2300  CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA 2603_al2.seq
2300  CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA 18rs21_al2.seq
2301  CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA 515_al2.seq
2300  CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA cjb111_al2.seq
2300  CATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCA h36b_al2.seq

      TTTTTAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTAC Majority
               2360      2370      2380      2390      2400
2350  TTTTTAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTAC 2603_al2.seq
2350  TTTTTAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTAC 18rs21_al2.seq
2351  TTTTTAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTAC 515_al2.seq
2350  TTTTTAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTAC cjb111_al2.seq
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      TCCGGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAATAAGTT Majority
               2410      2420      2430      2440      2450
2400  TCCGGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAATAAGTT 2603_al2.seq
2400  TCCGGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAATAAGTT 18rs21_al2.seq
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2400  TCCGGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAATAAGTT cjb111_al2.seq
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      TTAATCGGCCTGTTTCAACTTTTCGCTTAGGATTTATCTGTAATTGATTT Majority
               2460      2470      2480      2490      2500
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               2510      2520      2530      2540      2550
2500  GATAACTTATCATCTGGTAATTCAATATAAAAAGGTACTATTGTTGAAAC 2603_al2.seq
2500  GATAACTTATCATCTGGTAATTCAATATAAAAAGGTACTATTGTTGAAAC 18rs21_al2.seq
2501  GATAACTTATCATCTGGTAATTCAATATAAAAAGGTACTATTGTTGAAAC 515_al2.seq
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               2560      2570      2580      2590      2600
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2550  GCTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGAGTG 18rs21_al2.seq
2551  GCTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGAGTG 515_al2.seq
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2550  GCTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGAGTG h36b_al2.seq

      CTATCTTTGTCTGACCATTAGTATCAGTAGGAGAAGTCAAGATACTCTTA Majority
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2600  CTATCTTTGTCTGACCATTAGTATCAGTAGGAGAAGTCAAGATACTCTTA 18rs21_al2.seq
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      TACTTCTGGTTCAATTCGCTATCTGTCATTTGGCTCAATAAATCAACTTT Majority
               2660      2670      2680      2690      2700
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```

FIGURE 19E

```
     TAAGTTGTCAGTCACAGTCCATAAACGATAAGAAATCCCCTCCTCTGTAG Majority
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2700 TAAGTTGTCAGTCACAGTCCATAAACGATAAGAAATCCCCTCCTCTGTAG 18rs21_a12.seq
2701 TAAGTTGTCAGTCACAGTCCATAAACGATAAGAAATCCCCTCCTCTGTAG 515_a12.seq
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     TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA Majority
              2760      2770      2780      2790      2800
2750 TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA 2603_a12.seq
2750 TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA 18rs21_a12.seq
2751 TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA 515_a12.seq
2750 TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA cjb111_a12.seq
2750 TATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGTATCA h36b_a12.seq

     GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA Majority
              2810      2820      2830      2840      2850
2800 GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA 2603_a12.seq
2800 GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA 18rs21_a12.seq
2801 GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA 515_a12.seq
2800 GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA cjb111_a12.seq
2800 GCATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAA h36b_a12.seq

     GCAACATAGTAGAAGTCCTAAACTTTTTCTAATCTTTTTCATTTTTGATT Majority
              2860      2870      2880      2890      2900
2850 GCAACATAGTAGAAGTCCTAAACTTTTTCTAATCTTTTTCATTTTTGATT 2603_a12.seq
2850 GCAACATAGTAGAAGTCCTAAACTTTTTCTAATCTTTTTCATTTTTGATT 18rs21_a12.seq
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     TCCCTTTCTCTTTCTCTCTTTAAATTTTCGTTTTAAATATAATAGTAAAG Majority
              2910      2920      2930      2940      2950
2900 TCCCTTTCTCTTTCTCTCTTTAAATTTTCGTTTTAAATATAATAGTAAAG 2603_a12.seq
2900 TCCCTTTCTCTTTCTCTCTTTAAATTTTCGTTTTAAATATAATAGTAAAG 18rs21_a12.seq
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2900 TCCCTTTCTTTTTCTCTCTTTAAATTTTCGTTTTAAATATAATAGTAAAG h36b_a12.seq

     CGACTAATATAAGAATAACTAGGATTGATAAGAGGAAATAAAGTTTATAG Majority
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     TGTGTTTGCAATTCTTTCATTAAATAGTTCTTTTCTTTAACAGGAGGTAC Majority
              3010      3020      3030      3040      3050
3000 TGTGTTTGCAATTCTTTCATTAAATAGTTCTTTTCTTTAACAGGAGGTAC 2603_a12.seq
3000 TGTGTTTGCAATTCTTTCATTAAATAGTTCTTTTCTTTAACAGGAGGTAC 18rs21_a12.seq
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     ATACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAAT Majority
              3060      3070      3080      3090      3100
3050 ATACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAAT 2603_a12.seq
3050 ATACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAAT 18rs21_a12.seq
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     AAGGTGTACATGTTAGCAAAGTCGCATAATCCTTACCTTTAACAACCAAT Majority
              3110      3120      3130      3140      3150
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3100 AAGGTGTACATGTTAGCAAAGTCGCATAATCCTTACCTTTAACAACCAAT 18rs21_a12.seq
3101 AAGGTGTACATGTTAGCAAAGTCGCATAATCCTTACCTTTAACAACCAAT 515_a12.seq
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FIGURE 19F

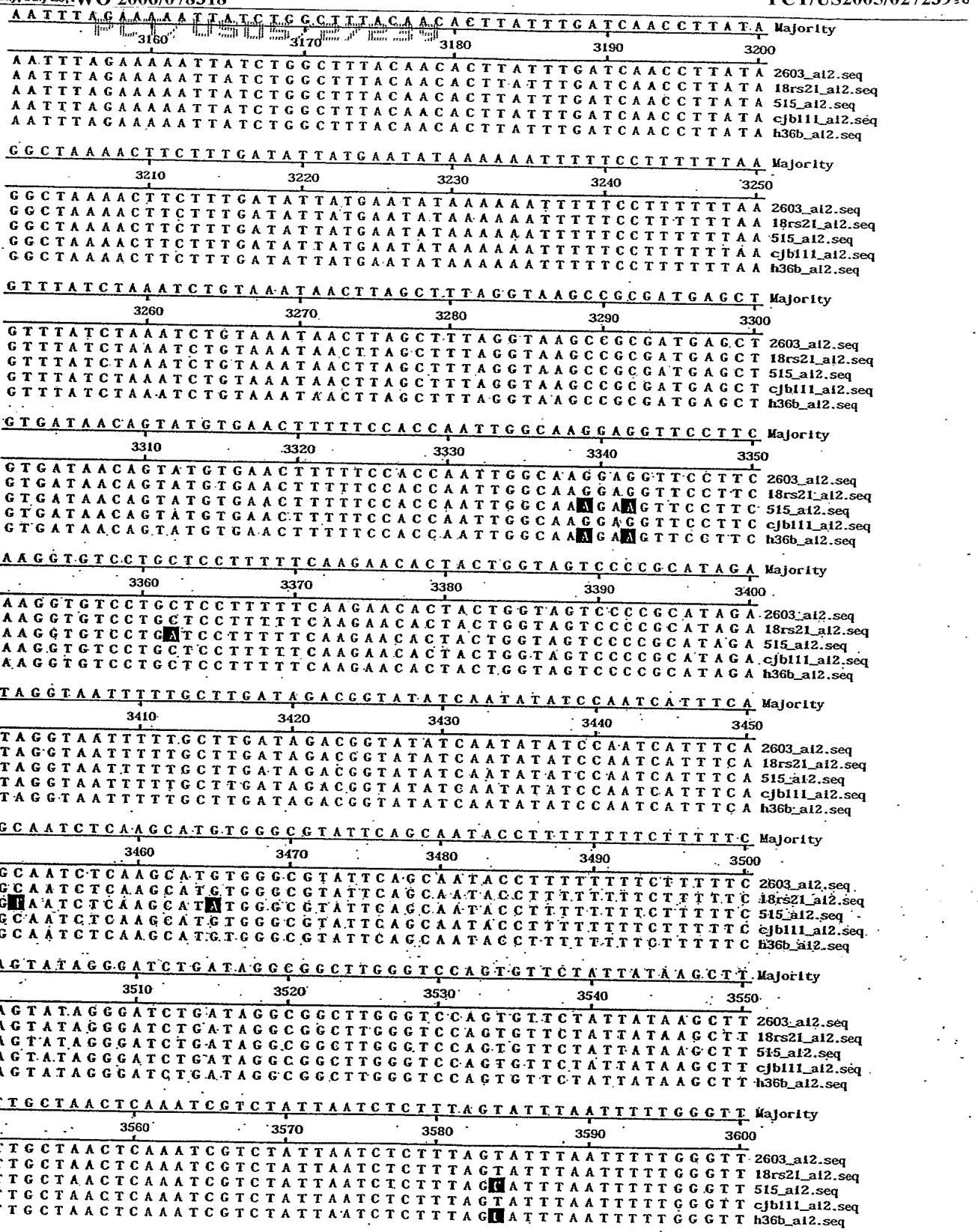
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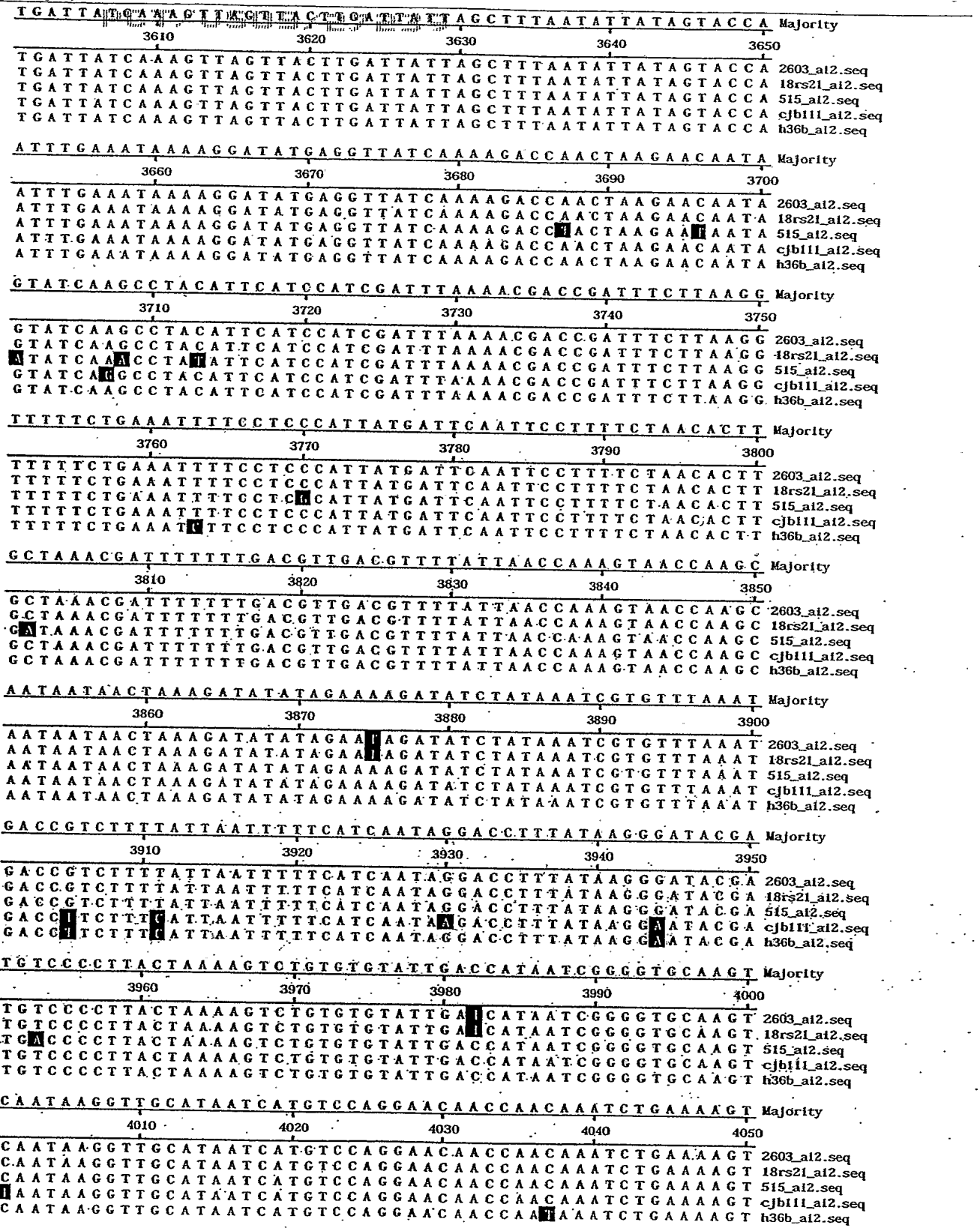
FIGURE 19G


Majority
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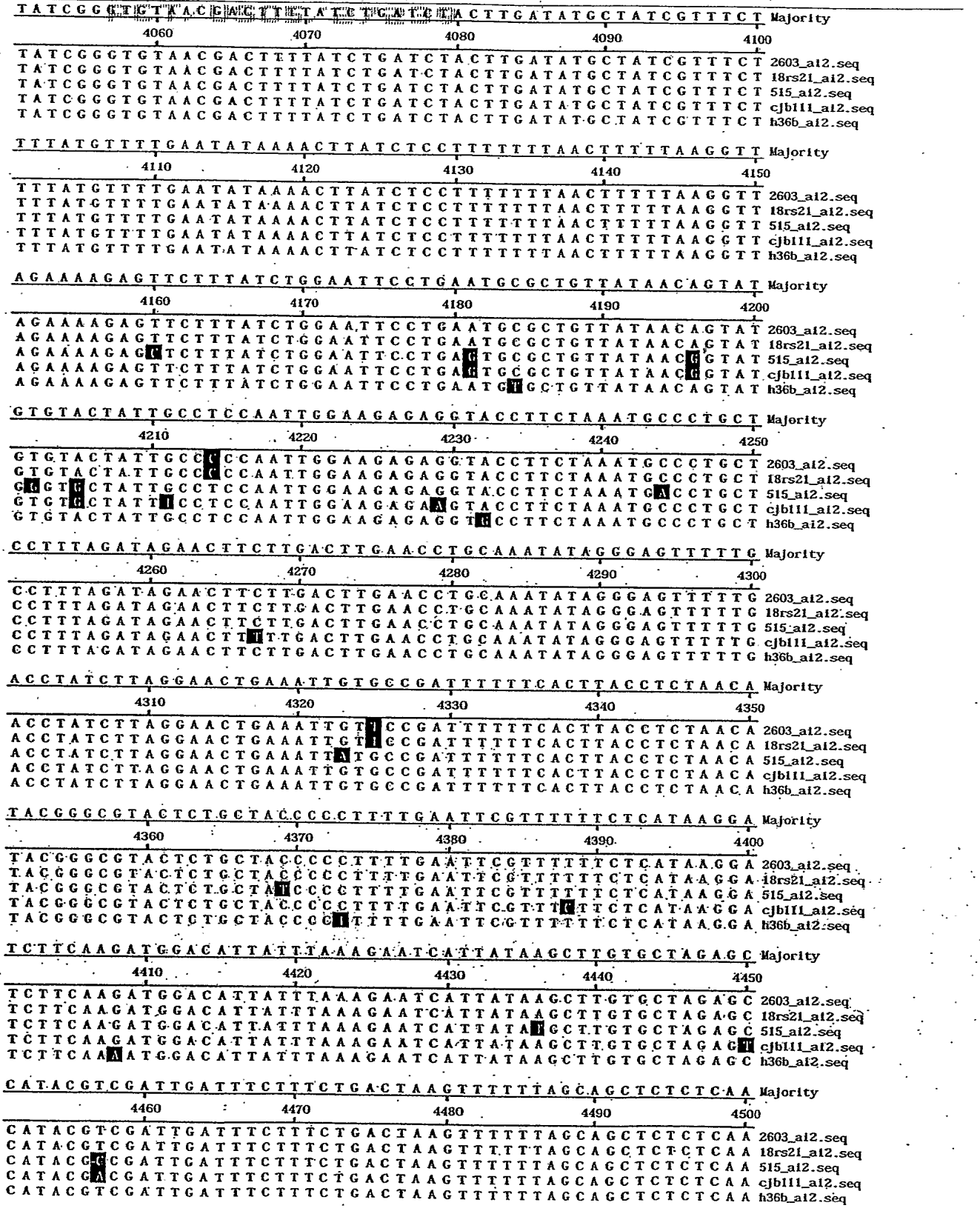
cjb111_a12.seq
h36b_a12.seq

FIGURE 19H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4060 4070 4080 4090 4100
4050 TATCGGGTGTAACGACTTTTATCTGATCTACTTGATATGCTATCGTTTCT 2603_a12.seq
4050 TATCGGGTGTAACGACTTTTATCTGATCTACTTGATATGCTATCGTTTCT 18rs21_a12.seq
4051 TATCGGGTGTAACGACTTTTATCTGATCTACTTGATATGCTATCGTTTCT 515_a12.seq
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4050 TATCGGGTGTAACGACTTTTATCTGATCTACTTGATATGCTATCGTTTCT h36b_a12.seq
TTTATGTTTTGAATATAAAACTTATCTCCTTTTTTTAACTTTTTAAGGTT Majority
4110 4120 4130 4140 4150
4100 TTTATGTTTTGAATATAAAACTTATCTCCTTTTTTTAACTTTTTAAGGTT 2603_a12.seq
4100 TTTATGTTTTGAATATAAAACTTATCTCCTTTTTTTAACTTTTTAAGGTT 18rs21_a12.seq
4101 TTTATGTTTTGAATATAAAACTTATCTCCTTTTTTTAACTTTTTAAGGTT 515_a12.seq
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4150 AGAAAAGAGTTCTTTATCTGGAATTCCTGAATGCGCTGTTATAACAGTAT 2603_a12.seq
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4150 AGAAAAGAGTTCTTTATCTGGAATTCCTGAGTGCGCTGTTATAACGGTAT cjb111_a12.seq
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4200 GTGTACTATTGCCCCCAATTGGAAGAGAGGTACCTTCTAAATGCCCTGCT 2603_a12.seq
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4201 GCGTGCTATTGCCTCCAATTGGAAGAGAGGTACCTTCTAAATGACCTGCT 515_a12.seq
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4250 CCTTTAGATAGAACTTCTTGACTTGAACCTGCAAATATAGGGAGTTTTTG 2603_a12.seq
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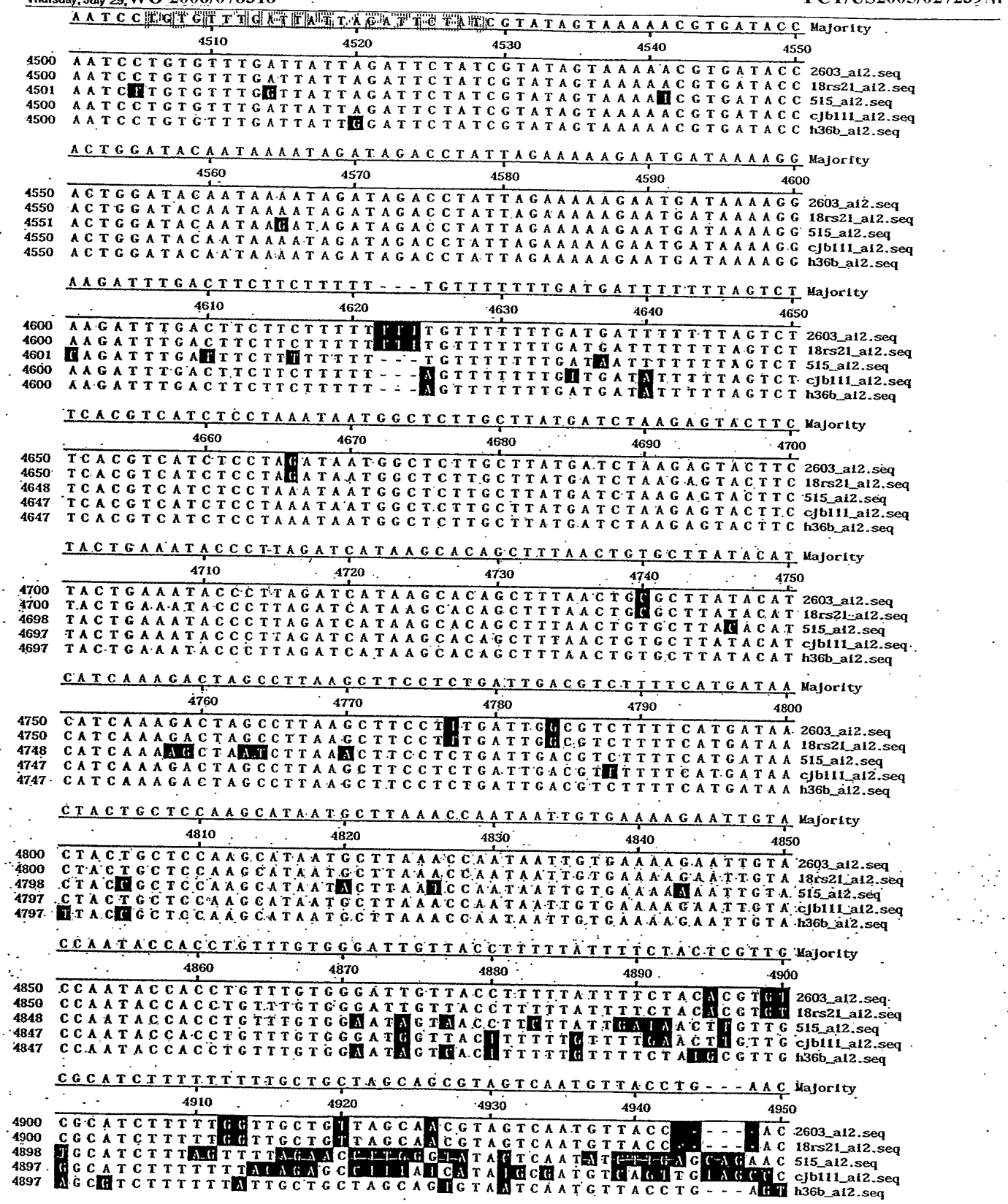
FIGURE 191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h36b_a12.seq

FIGURE 19J

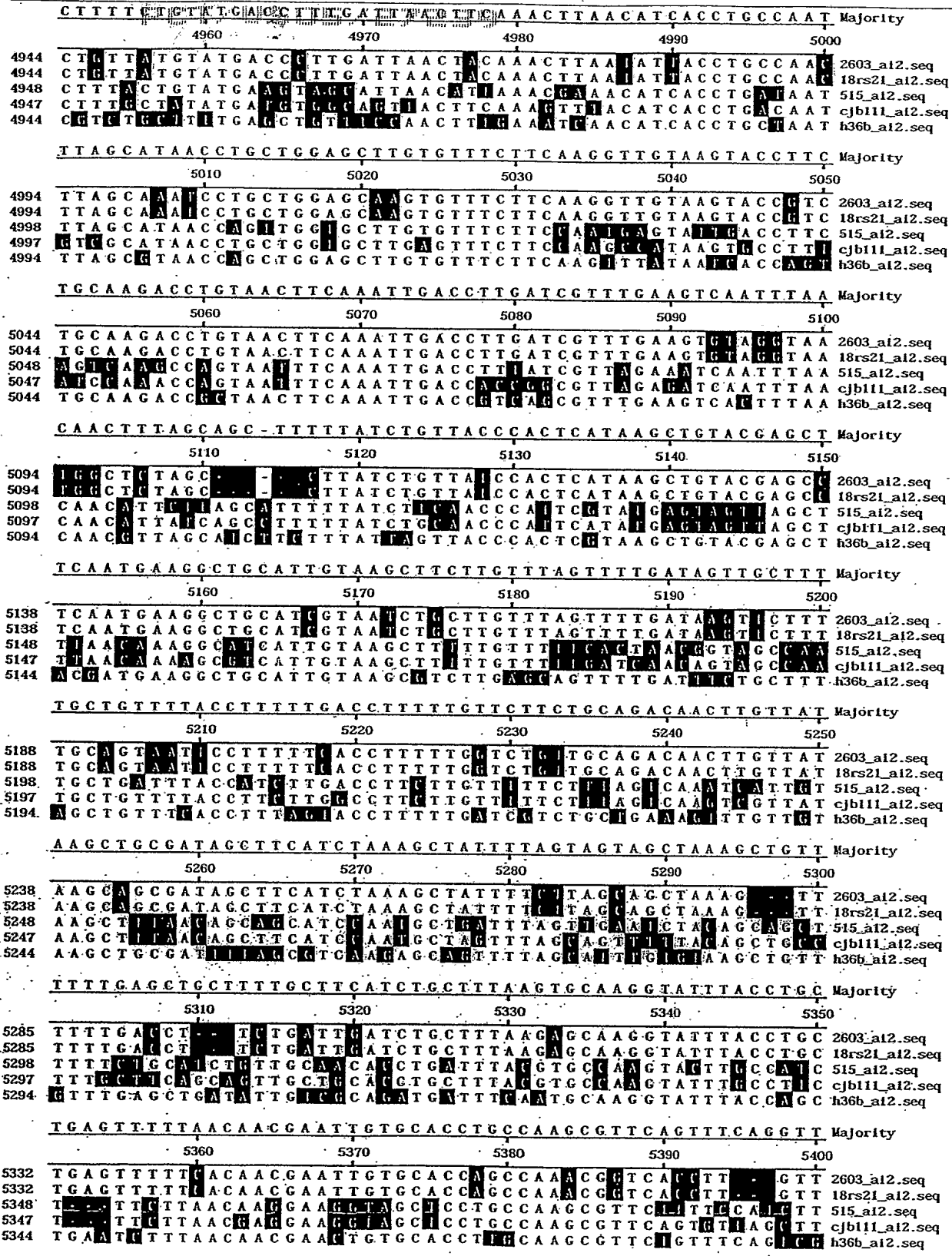
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FIGURE 19K

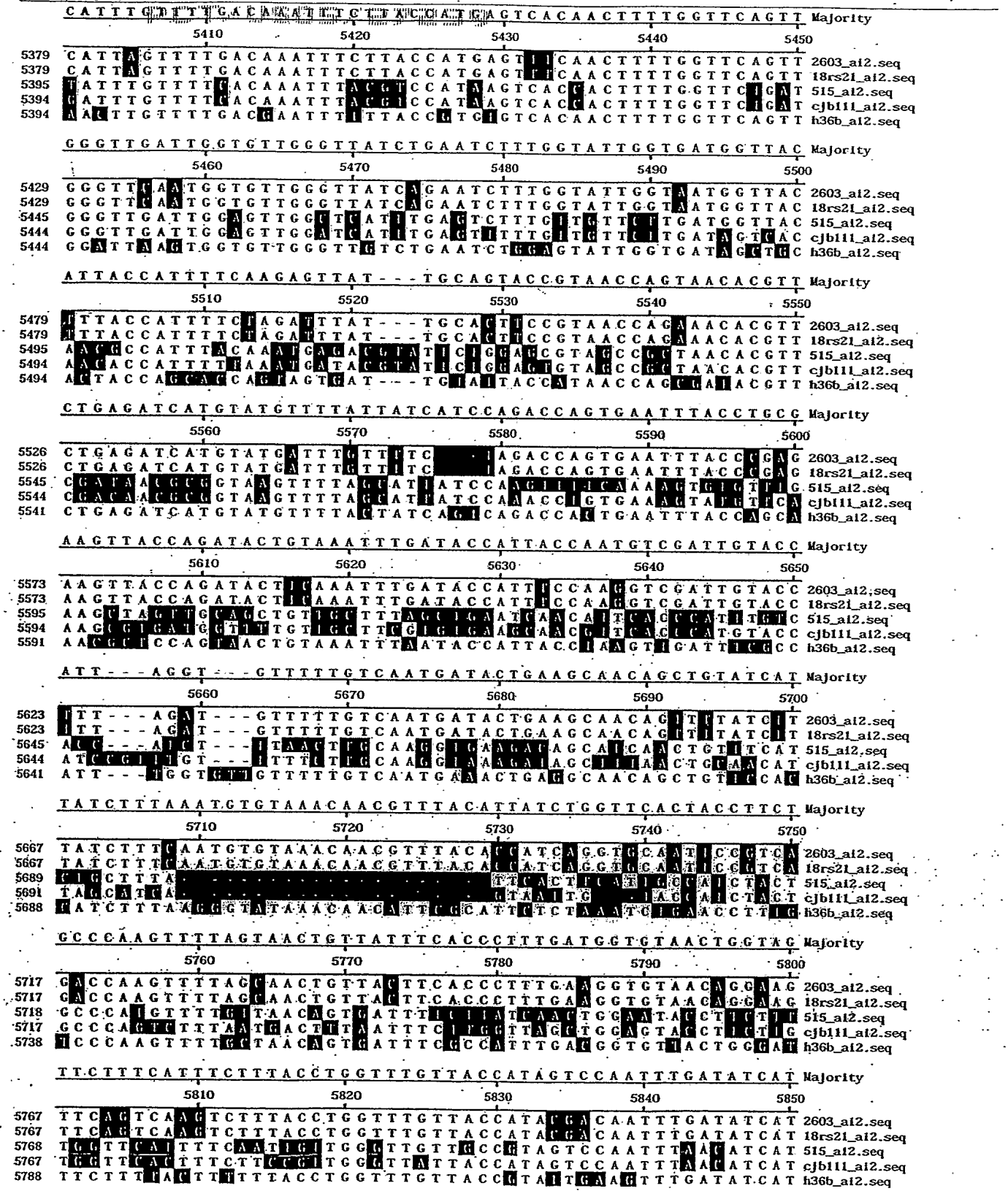
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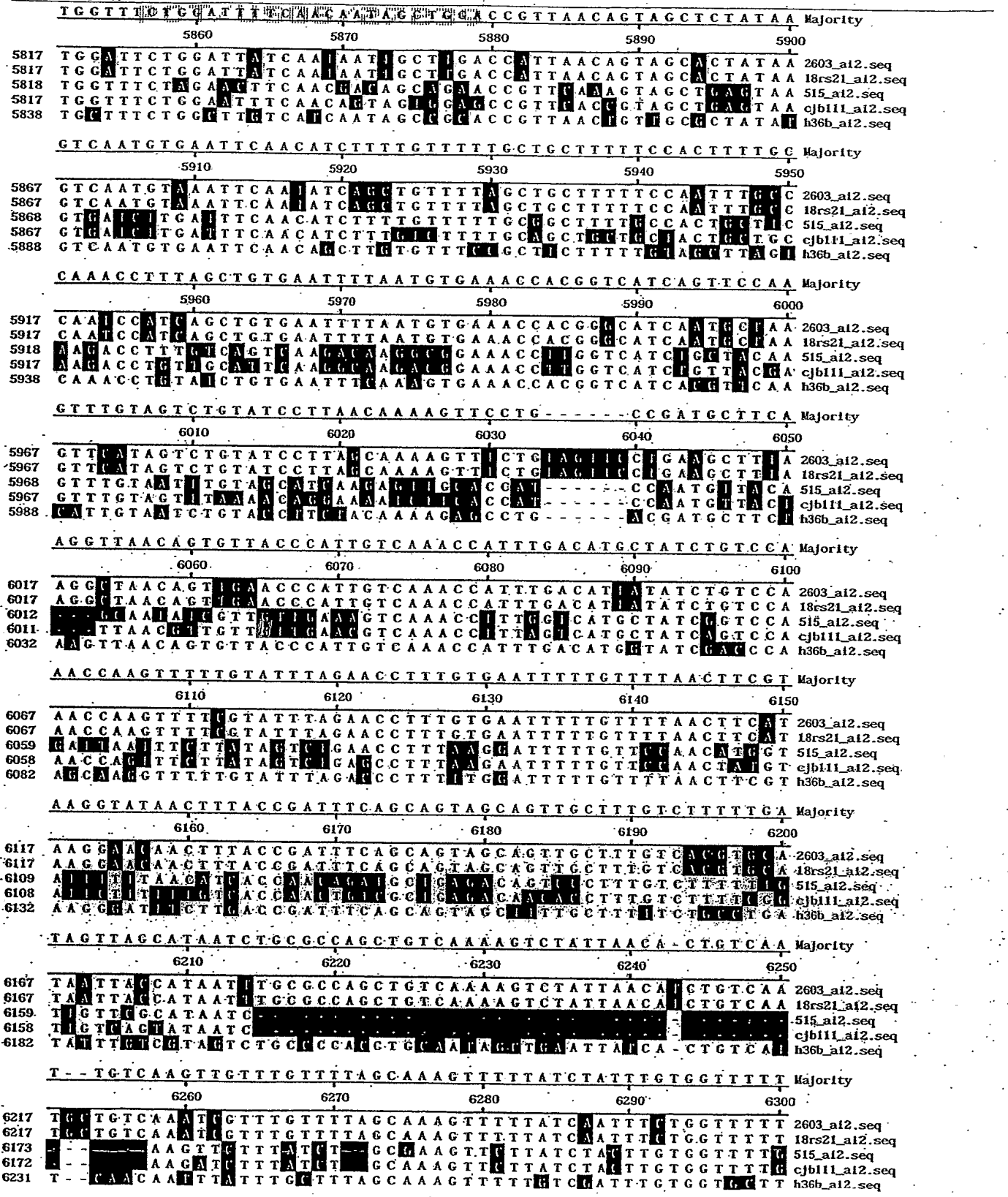
FIGURE 19L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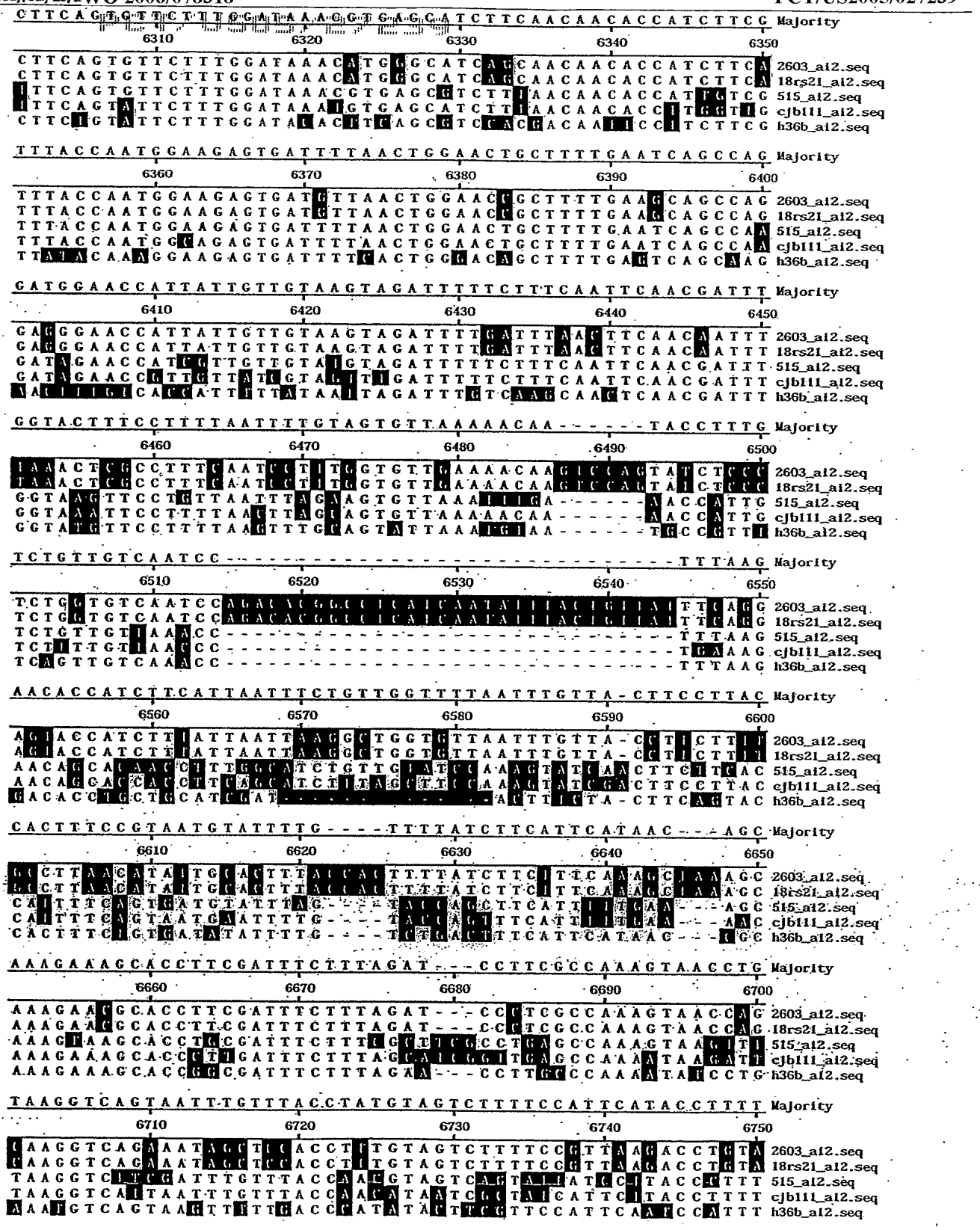
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19M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515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19N

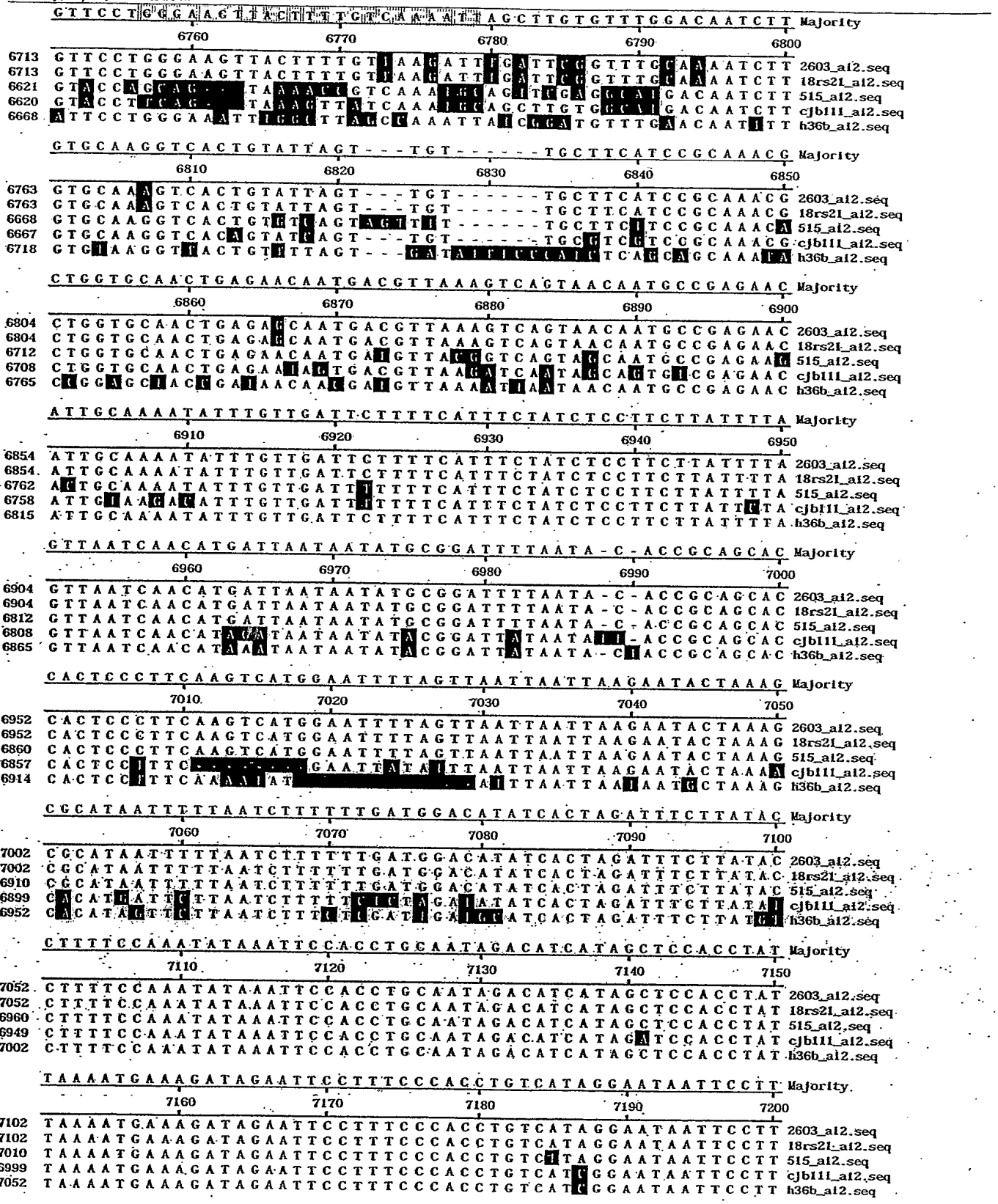
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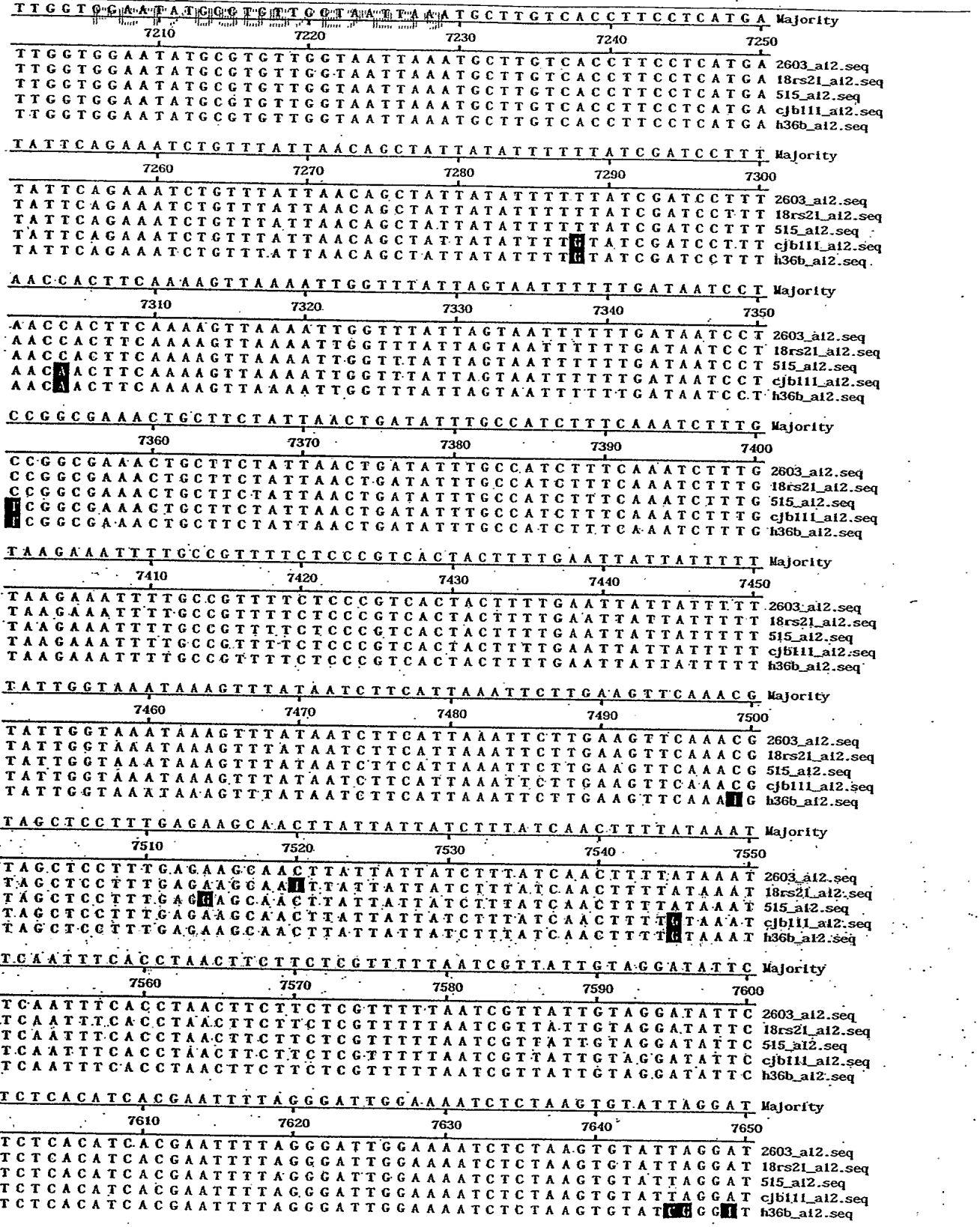
FIGURE 19O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cjb111_a12.seq
h36b_a12.seq

FIGURE 19P

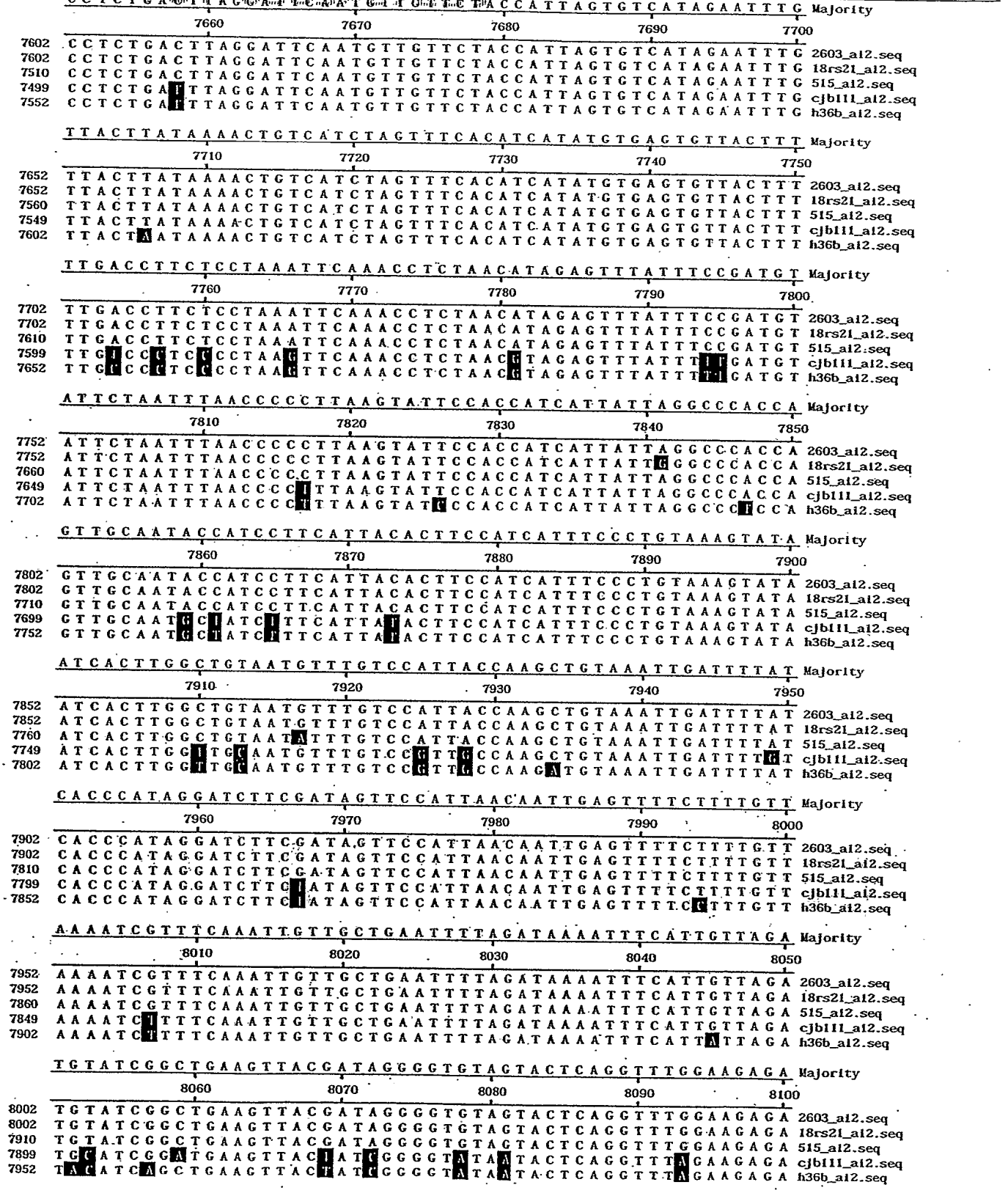
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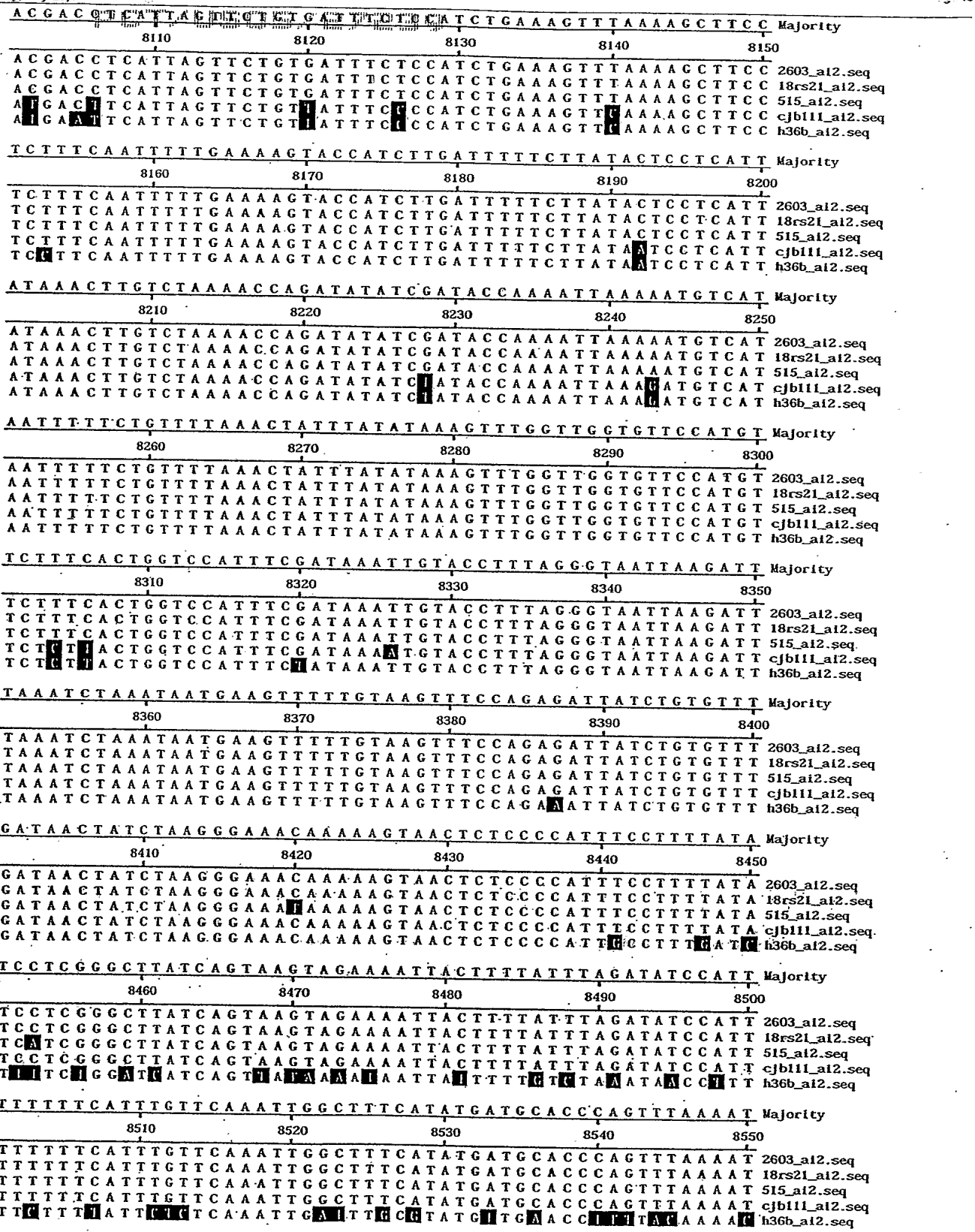
FIGURE 19Q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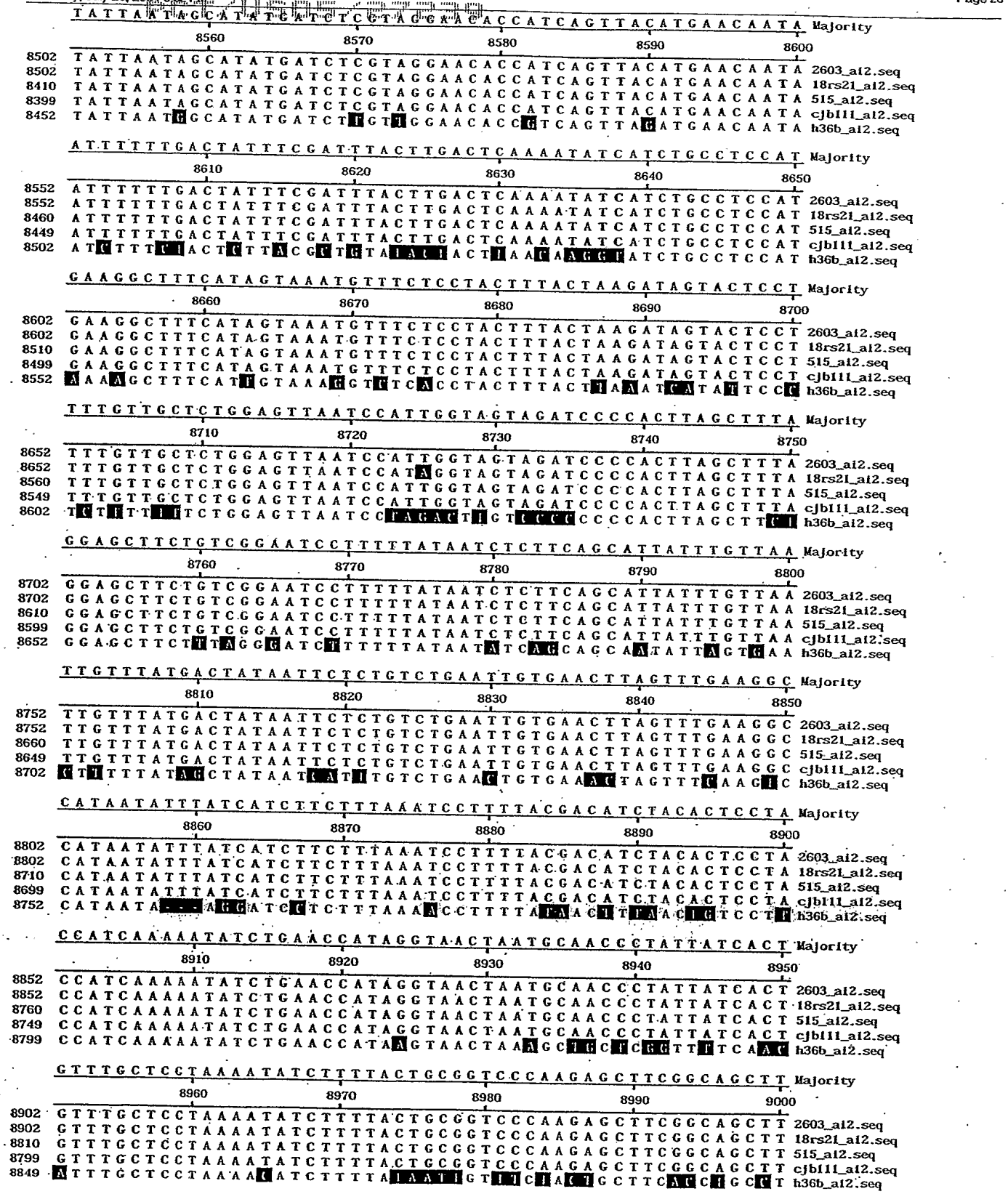
8510 8520 8530 8540 8550

FIGURE 19R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8760 CCATCAAAAATATCTGAACCATAGGTAACTAATGCAACCCTATTATCACT 515_al2.seq
8749 CCATCAAAAATATCTGAACCATAGGTAACTAATGCAACCCTATTATCACT cjb111_al2.seq
8799 CCATCAAAAATATCTGAACCATAAGTAACTAAAGCTGCTCGGTTTCAAG h36b_al2.seq
GTTTGCTCCTAAAATATCTTTTACTGCGGTCCCAAGAGCTTCGGCAGCTT Majority
8960 8970 8980 8990 9000
8902 GTTTGCTCCTAAAATATCTTTTACTGCGGTCCCAAGAGCTTCGGCAGCTT 2603_al2.seq
8902 GTTTGCTCCTAAAATATCTTTTACTGCGGTCCCAAGAGCTTCGGCAGCTT 18rs21_al2.seq
8810 GTTTGCTCCTAAAATATCTTTTACTGCGGTCCCAAGAGCTTCGGCAGCTT 515_al2.seq
8799 GTTTGCTCCTAAAATATCTTTTACTGCGGTCCCAAGAGCTTCGGCAGCTT cjb111_al2.seq
8849 ATTTGCTCCTAAAACATCTTTTAIAATIGTTTCIACTGCTTCACCIGCCT h36b_al2.seq

FIGURE 19S

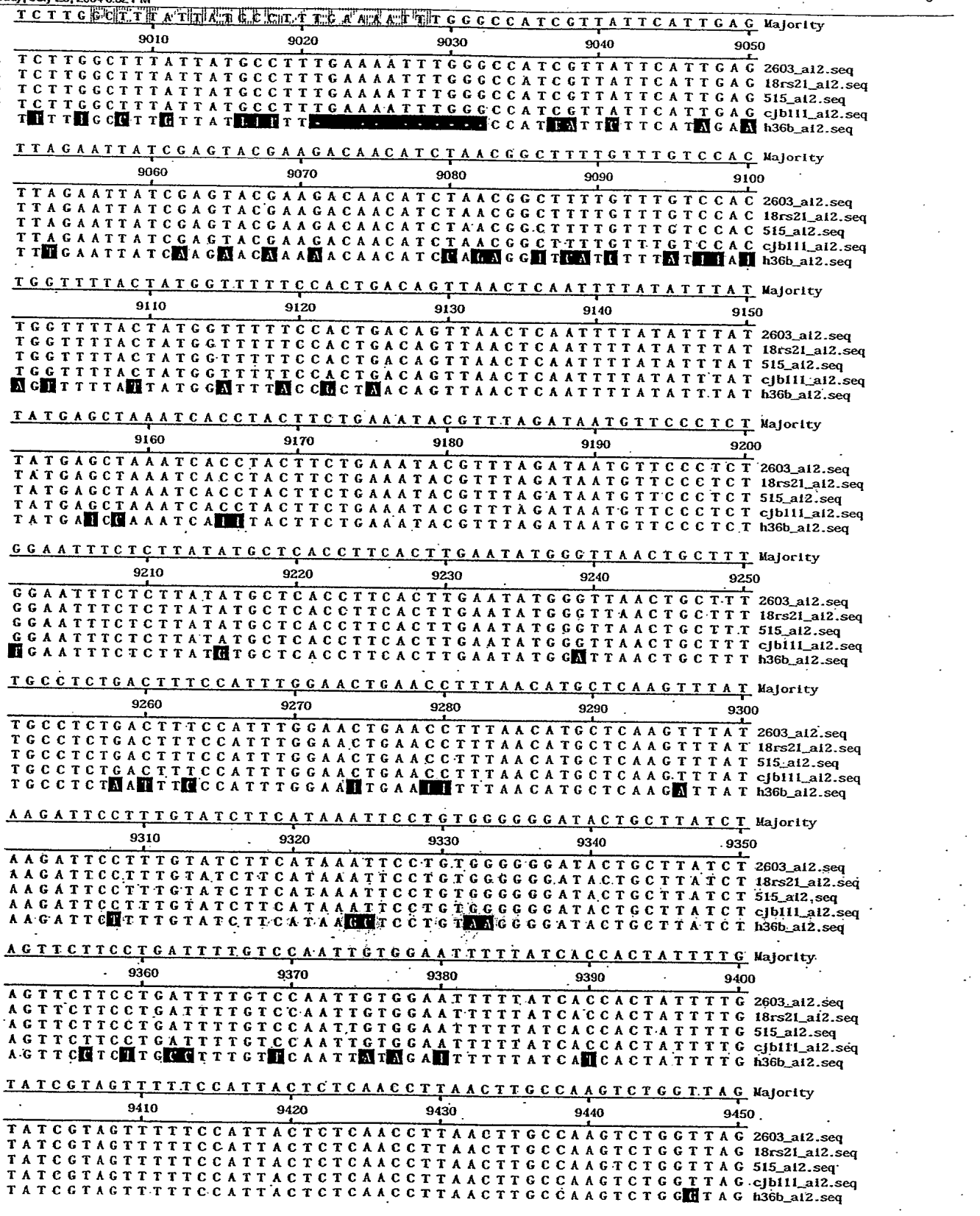

Majority
9010 9020 9030 9040 9050
9060 9070 9080 9090 9100
9110 9120 9130 9140 9150
9160 9170 9180 9190 9200
9210 9220 9230 9240 9250
9260 9270 9280 9290 9300
9310 9320 9330 9340 9350
9360 9370 9380 9390 9400
9410 9420 9430 9440 9450
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19T

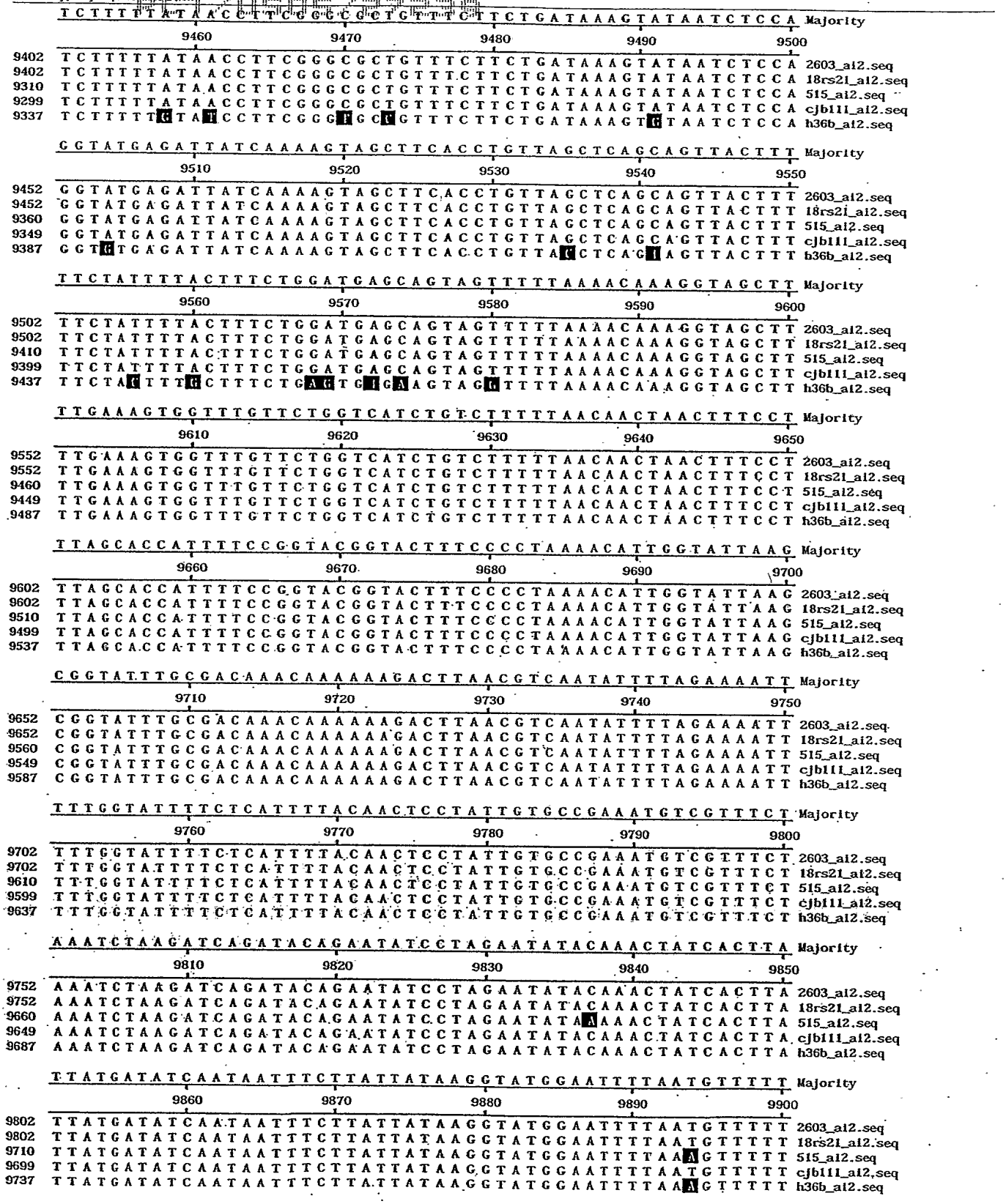

TCTTTTTATAACCTTCGGGCCGCTGTTTCTTCTGATAAAGTATAATCTCCA Majority
9460 9470 9480 9490 9500
9402 TCTTTTTATAACCTTCGGGCCGCTGTTTCTTCTGATAAAGTATAATCTCCA 2603_a12.seq
9402 TCTTTTTATAACCTTCGGGCCGCTGTTTCTTCTGATAAAGTATAATCTCCA 18rs21_a12.seq
9310 TCTTTTTATAACCTTCGGGCCGCTGTTTCTTCTGATAAAGTATAATCTCCA 515_a12.seq
9299 TCTTTTTATAACCTTCGGGCCGCTGTTTCTTCTGATAAAGTATAATCTCCA cjb111_a12.seq
9337 TCTTTTTGTATCCTTCGGGTGCGTTTCTTCTGATAAAGTGTAATCTCCA h36b_a12.seq
GGTATGAGATTATCAAAAGTAGCTTCACCTGTTAGCTCAGCAGTTACTTT Majority
9510 9520 9530 9540 9550
9452 GGTATGAGATTATCAAAAGTAGCTTCACCTGTTAGCTCAGCAGTTACTTT 2603_a12.seq
9452 GGTATGAGATTATCAAAAGTAGCTTCACCTGTTAGCTCAGCAGTTACTTT 18rs21_a12.seq
9360 GGTATGAGATTATCAAAAGTAGCTTCACCTGTTAGCTCAGCAGTTACTTT 515_a12.seq
9349 GGTATGAGATTATCAAAAGTAGCTTCACCTGTTAGCTCAGCAGTTACTTT cjb111_a12.seq
9387 GGTGTGAGATTATCAAAAGTAGCTTCACCTGTTACCTCAGTAGTTACTTT h36b_a12.seq
TTCTATTTTACTTTCTGGATGAGCAGTAGTTTTTAAAACAAAGGTAGCTT Majority
9560 9570 9580 9590 9600
9502 TTCTATTTTACTTTCTGGATGAGCAGTAGTTTTTAAAACAAAGGTAGCTT 2603_a12.seq
9502 TTCTATTTTACTTTCTGGATGAGCAGTAGTTTTTAAAACAAAGGTAGCTT 18rs21_a12.seq
9410 TTCTATTTTACTTTCTGGATGAGCAGTAGTTTTTAAAACAAAGGTAGCTT 515_a12.seq
9399 TTCTATTTTACTTTCTGGATGAGCAGTAGTTTTTAAAACAAAGGTAGCTT cjb111_a12.seq
9437 TTCTACTTTTGCTTTCTGAGTGTGAAGTAGGTTTTTAAAACAAAGGTAGCTT h36b_a12.seq
TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT Majority
9610 9620 9630 9640 9650
9552 TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT 2603_a12.seq
9552 TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT 18rs21_a12.seq
9460 TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT 515_a12.seq
9449 TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT cjb111_a12.seq
9487 TTGAAAGTGGTTTGTTCTGGTCATCTGTCTTTTTAACAACTAACTTTCCT h36b_a12.seq
TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG Majority
9660 9670 9680 9690 9700
9602 TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG 2603_a12.seq
9602 TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG 18rs21_a12.seq
9510 TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG 515_a12.seq
9499 TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG cjb111_a12.seq
9537 TTAGCACCATTTTCCGGTACGGTACTTTCCCCTAAAACATTGGTATTAAG h36b_a12.seq
CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT Majority
9710 9720 9730 9740 9750
9652 CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT 2603_a12.seq
9652 CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT 18rs21_a12.seq
9560 CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT 515_a12.seq
9549 CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT cjb111_a12.seq
9587 CGGTATTTGCGACAAACAAAAAAGACTTAACGTCAATATTTTAGAAAATT h36b_a12.seq
TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT Majority
9760 9770 9780 9790 9800
9702 TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT 2603_a12.seq
9702 TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT 18rs21_a12.seq
9610 TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT 515_a12.seq
9599 TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT cjb111_a12.seq
9637 TTTGGTATTTTCTCATTTTACAACTCCTATTGTGCCGAAATGTCGTTTCT h36b_a12.seq
AAATCTAAGATCAGATACAGAATATCCTAGAATATACAAACTATCACTTA Majority
9810 9820 9830 9840 9850
9752 AAATCTAAGATCAGATACAGAATATCCTAGAATATACAAACTATCACTTA 2603_a12.seq
9752 AAATCTAAGATCAGATACAGAATATCCTAGAATATACAAACTATCACTTA 18rs21_a12.seq
9660 AAATCTAAGATCAGATACAGAATATCCTAGAATATAAAACTATCACTTA 515_a12.seq
9649 AAATCTAAGATCAGATACAGAATATCCTAGAATATACAAACTATCACTTA cjb111_a12.seq
9687 AAATCTAAGATCAGATACAGAATATCCTAGAATATACAAACTATCACTTA h36b_a12.seq
TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAATGTTTTT Majority
9860 9870 9880 9890 9900
9802 TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAATGTTTTT 2603_a12.seq
9802 TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAATGTTTTT 18rs21_a12.seq
9710 TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAAAGTTTTT 515_a12.seq
9699 TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAATGTTTTT cjb111_a12.seq
9737 TTATGATATCAATAATTTCTTATTATAAGGTATGGAATTTTAAAGTTTTT h36b_a12.seq

FIGURE 19U

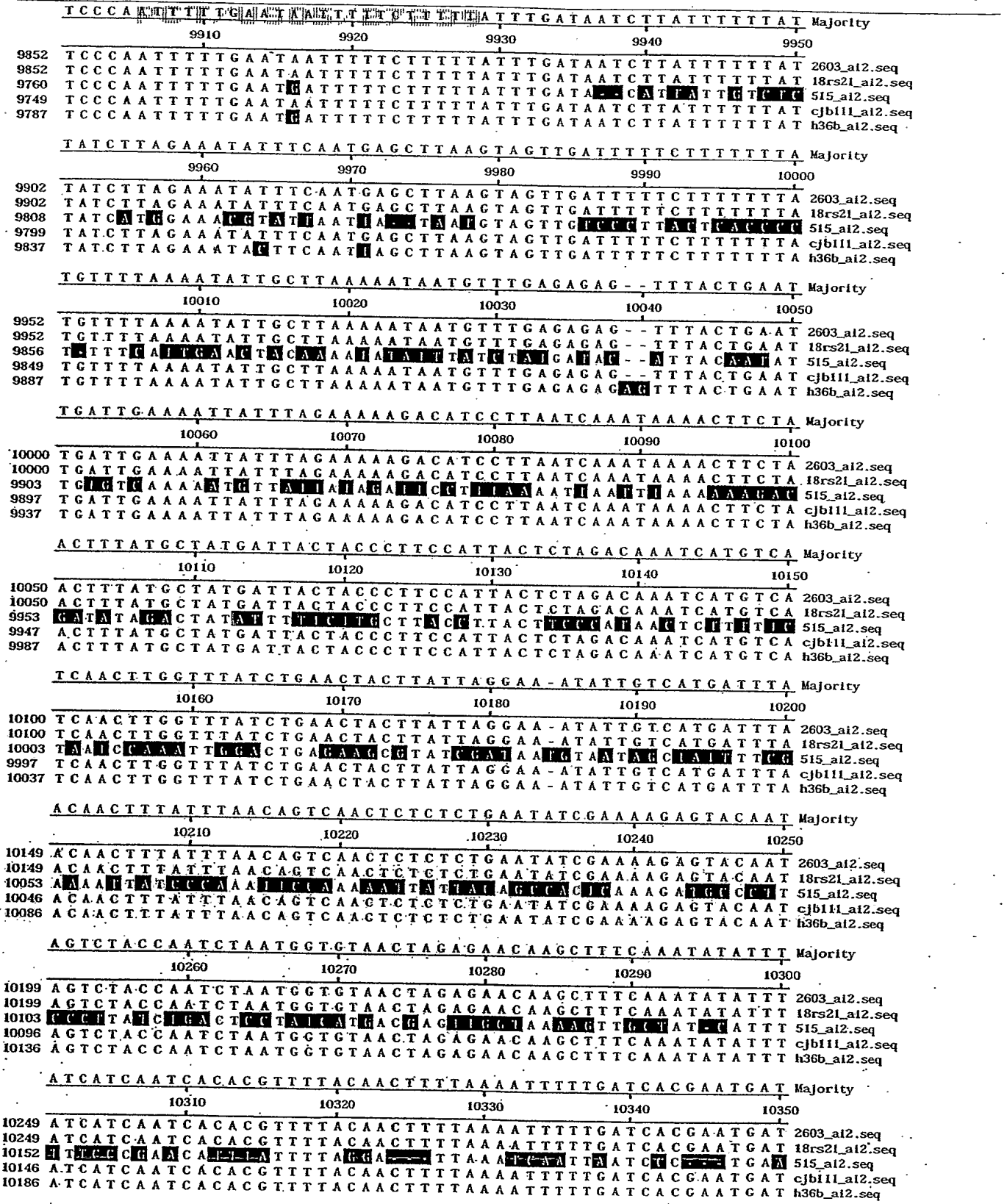

Majority
2603_al2.seq
18rs21_al2.seq
515_al2.seq
cjb111_al2.seq
h36b_al2.seq

FIGURE 19V

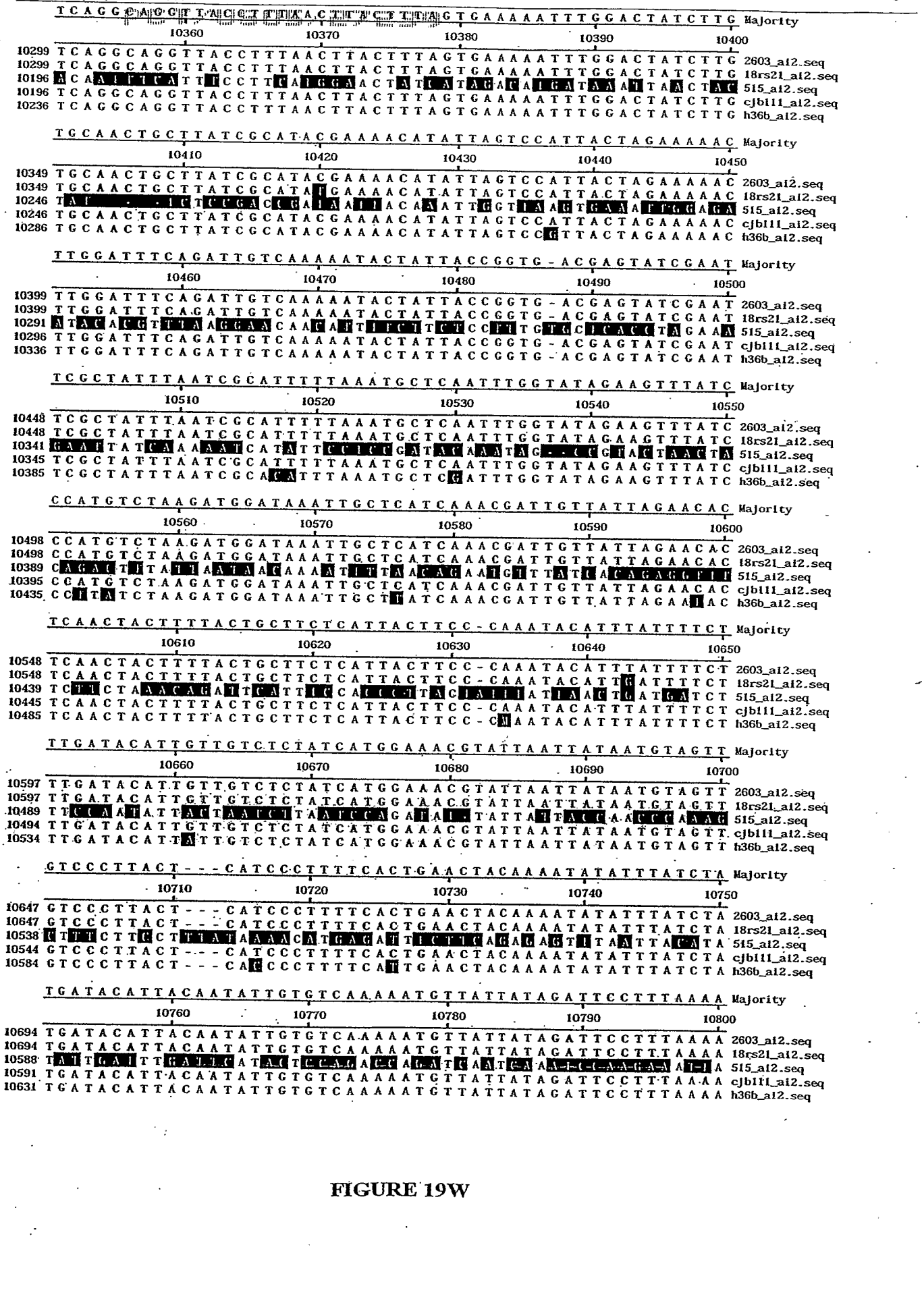

Majority
10360 10370 10380 10390 10400
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10410 10420 10430 10440 10450
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10460 10470 10480 10490 10500
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10510 10520 10530 10540 10550
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10560 10570 10580 10590 10600
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10610 10620 10630 10640 10650
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10660 10670 10680 10690 10700
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10710 10720 10730 10740 10750
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
Majority
10760 10770 10780 10790 10800
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19W

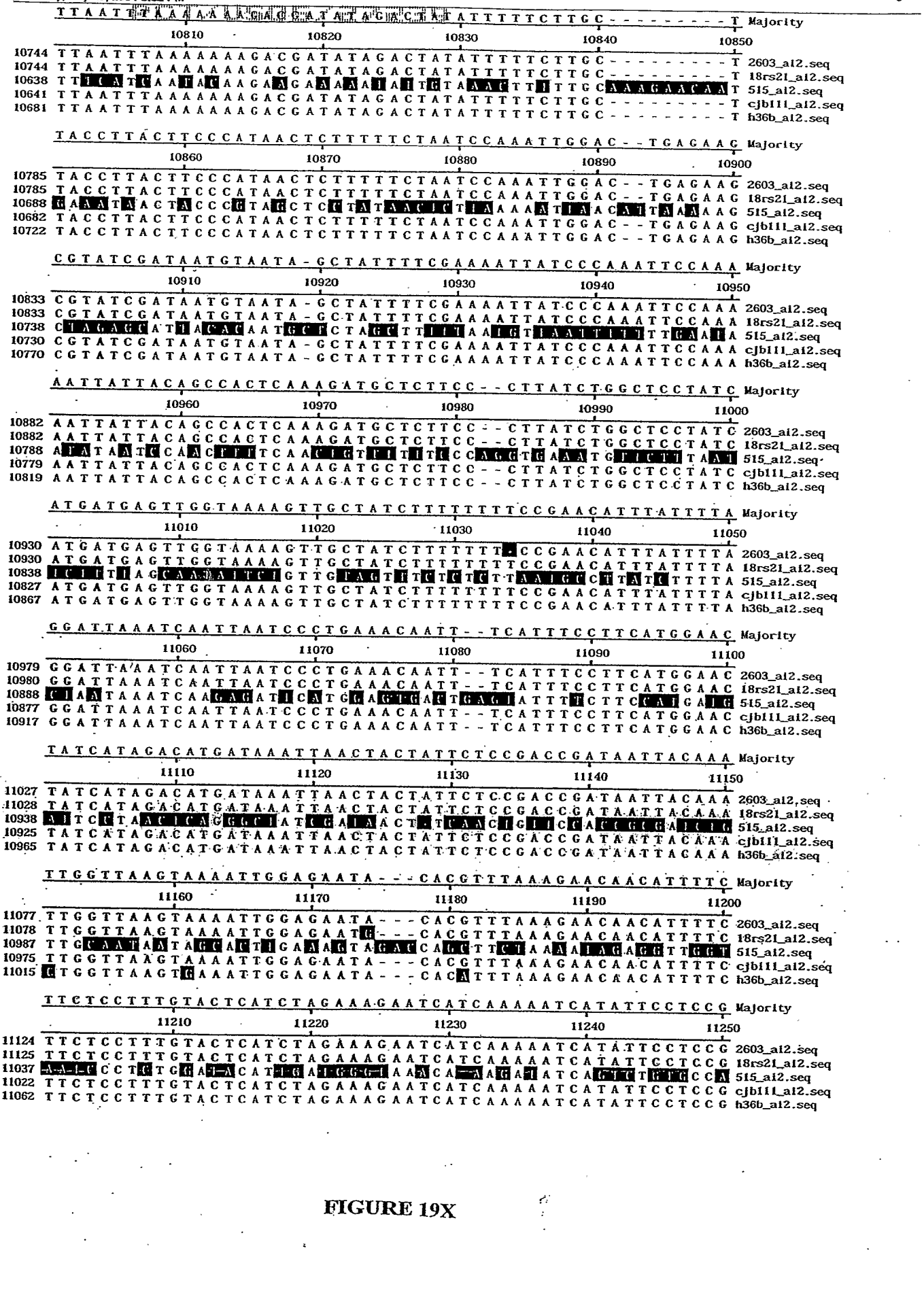

Majority
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19X

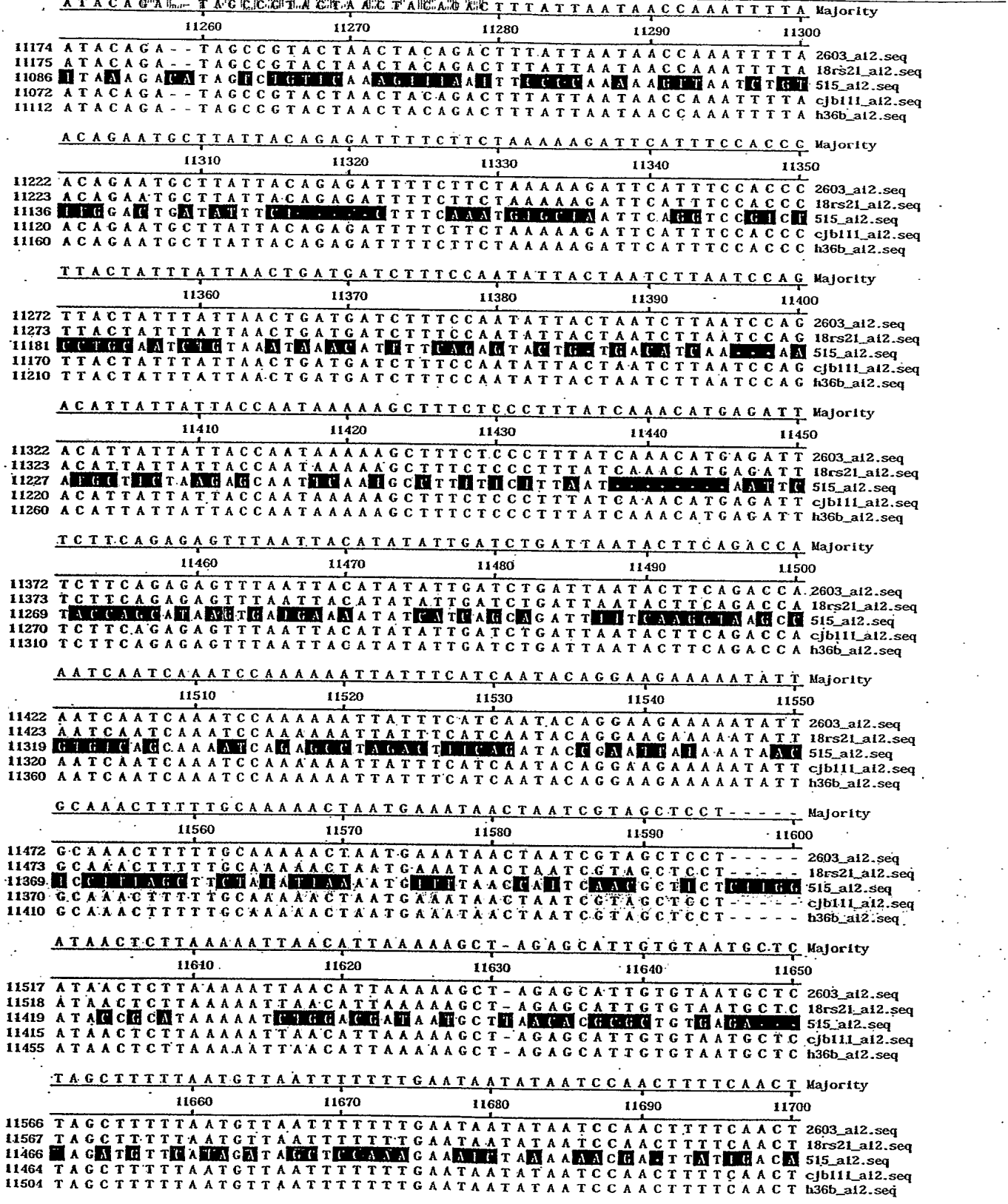

Majority
11260 11270 11280 11290 11300
11174 2603_a12.seq
11175 18rs21_a12.seq
11086 515_a12.seq
11072 cjb111_a12.seq
11112 h36b_a12.seq
Majority
11310 11320 11330 11340 11350
11222 2603_a12.seq
11223 18rs21_a12.seq
11136 515_a12.seq
11120 cjb111_a12.seq
11160 h36b_a12.seq
Majority
11360 11370 11380 11390 11400
11272 2603_a12.seq
11273 18rs21_a12.seq
11181 515_a12.seq
11170 cjb111_a12.seq
11210 h36b_a12.seq
Majority
11410 11420 11430 11440 11450
11322 2603_a12.seq
11323 18rs21_a12.seq
11227 515_a12.seq
11220 cjb111_a12.seq
11260 h36b_a12.seq
Majority
11460 11470 11480 11490 11500
11372 2603_a12.seq
11373 18rs21_a12.seq
11269 515_a12.seq
11270 cjb111_a12.seq
11310 h36b_a12.seq
Majority
11510 11520 11530 11540 11550
11422 2603_a12.seq
11423 18rs21_a12.seq
11319 515_a12.seq
11320 cjb111_a12.seq
11360 h36b_a12.seq
Majority
11560 11570 11580 11590 11600
11472 2603_a12.seq
11473 18rs21_a12.seq
11369 515_a12.seq
11370 cjb111_a12.seq
11410 h36b_a12.seq
Majority
11610 11620 11630 11640 11650
11517 2603_a12.seq
11518 18rs21_a12.seq
11419 515_a12.seq
11415 cjb111_a12.seq
11455 h36b_a12.seq
Majority
11660 11670 11680 11690 11700
11566 2603_a12.seq
11567 18rs21_a12.seq
11466 515_a12.seq
11464 cjb111_a12.seq
11504 h36b_a12.seq

FIGURE 19Y

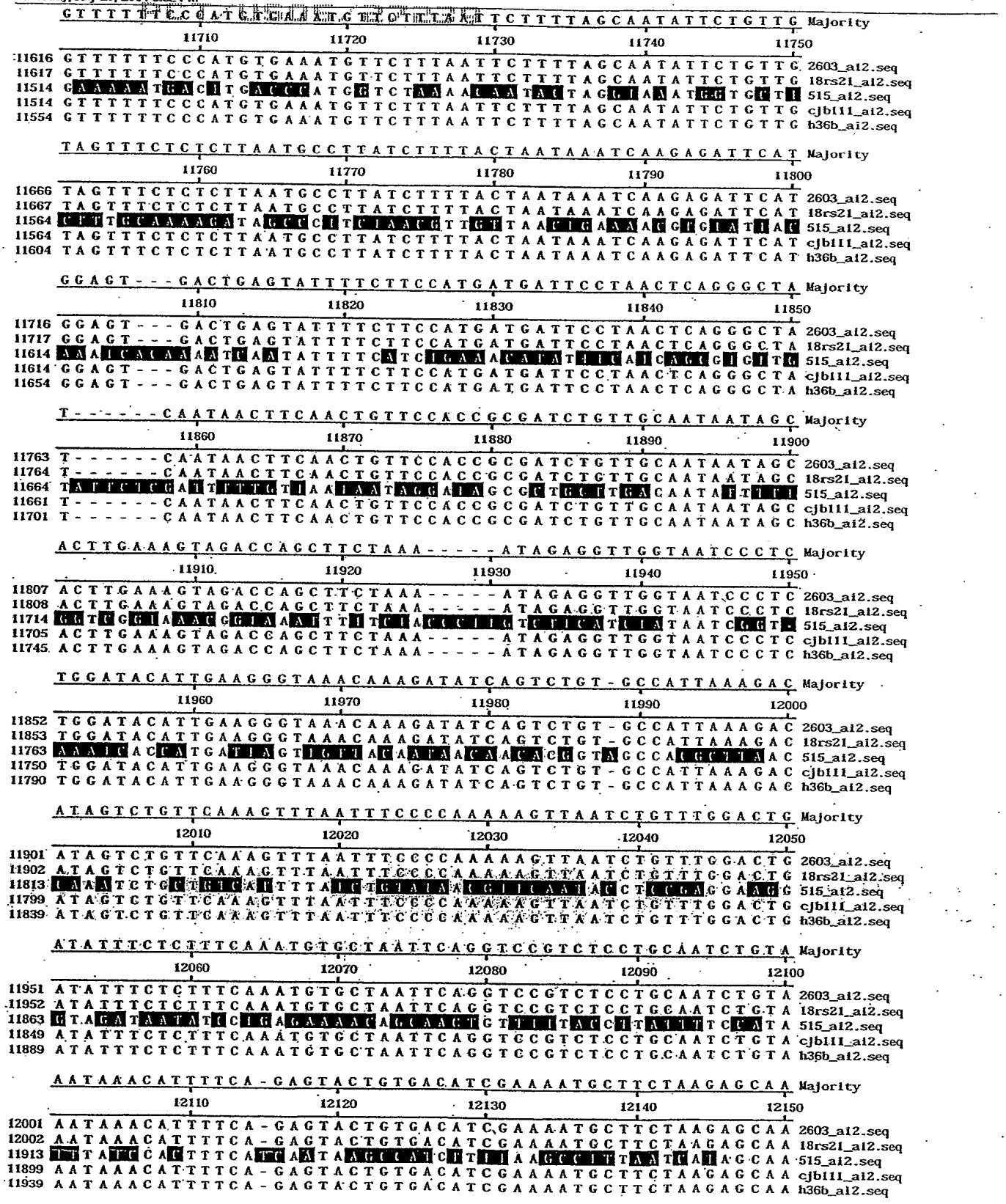

Majority
11710 11720 11730 11740 11750
11760 11770 11780 11790 11800
11810 11820 11830 11840 11850
11860 11870 11880 11890 11900
11910 11920 11930 11940 11950
11960 11970 11980 11990 12000
12010 12020 12030 12040 12050
12060 12070 12080 12090 12100
12110 12120 12130 12140 12150
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19Z

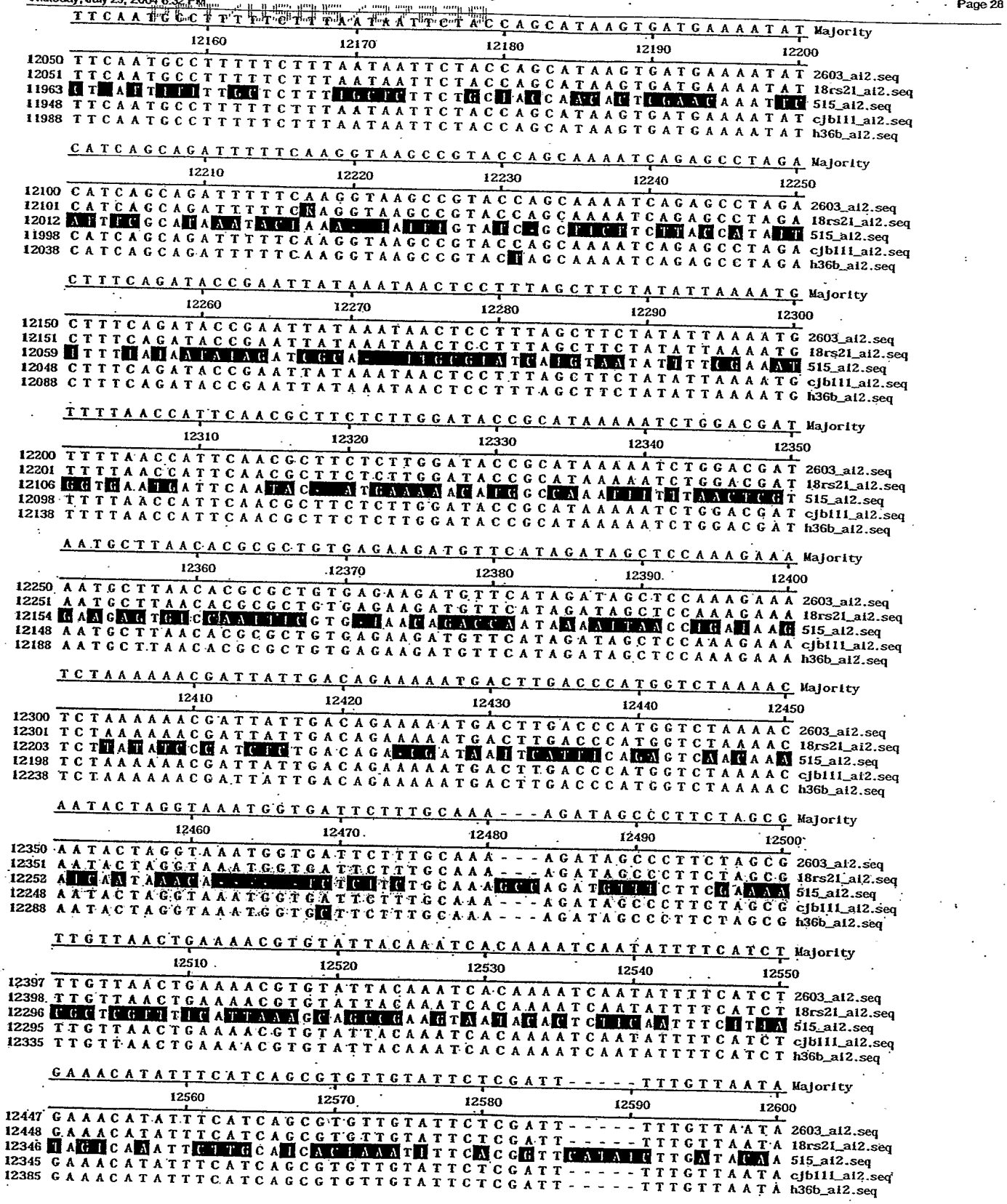

Majority
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19AA

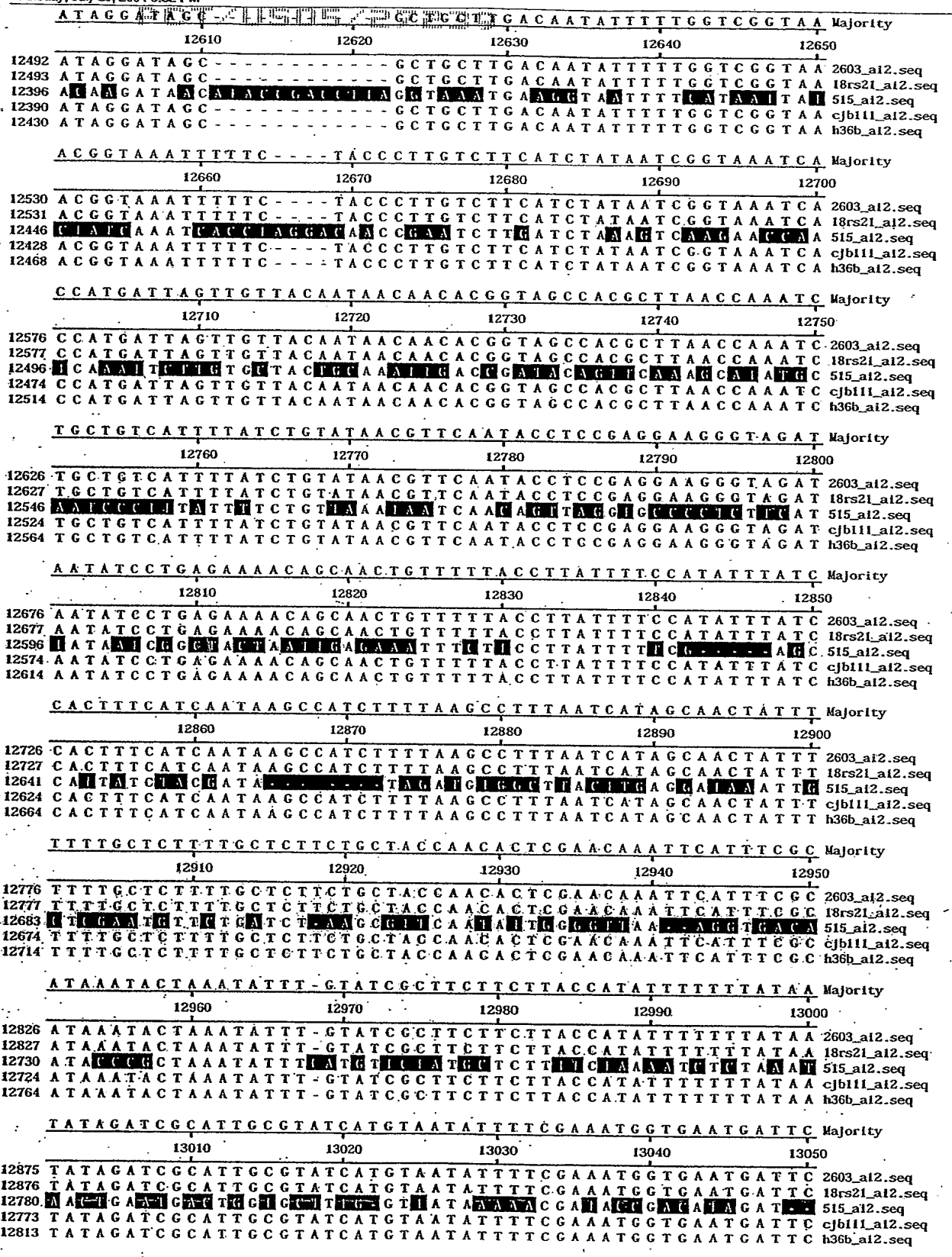

Majority
12610 12620 12630 12640 12650
12492 2603_a12.seq
12493 2603_a12.seq
12396 18rs21_a12.seq
12390 515_a12.seq
12430 cjb111_a12.seq
12430 h36b_a12.seq
Majority
12660 12670 12680 12690 12700
12530 2603_a12.seq
12531 2603_a12.seq
12446 18rs21_a12.seq
12428 515_a12.seq
12468 cjb111_a12.seq
12468 h36b_a12.seq
Majority
12710 12720 12730 12740 12750
12576 2603_a12.seq
12577 2603_a12.seq
12496 18rs21_a12.seq
12474 515_a12.seq
12514 cjb111_a12.seq
12514 h36b_a12.seq
Majority
12760 12770 12780 12790 12800
12626 2603_a12.seq
12627 2603_a12.seq
12546 18rs21_a12.seq
12524 515_a12.seq
12564 cjb111_a12.seq
12564 h36b_a12.seq
Majority
12810 12820 12830 12840 12850
12676 2603_a12.seq
12677 2603_a12.seq
12596 18rs21_a12.seq
12574 515_a12.seq
12614 cjb111_a12.seq
12614 h36b_a12.seq
Majority
12860 12870 12880 12890 12900
12726 2603_a12.seq
12727 2603_a12.seq
12641 18rs21_a12.seq
12624 515_a12.seq
12664 cjb111_a12.seq
12664 h36b_a12.seq
Majority
12910 12920 12930 12940 12950
12776 2603_a12.seq
12777 2603_a12.seq
12683 18rs21_a12.seq
12674 515_a12.seq
12714 cjb111_a12.seq
12714 h36b_a12.seq
Majority
12960 12970 12980 12990 13000
12826 2603_a12.seq
12827 2603_a12.seq
12730 18rs21_a12.seq
12724 515_a12.seq
12764 cjb111_a12.seq
12764 h36b_a12.seq
Majority
13010 13020 13030 13040 13050
12875 2603_a12.seq
12876 2603_a12.seq
12780 18rs21_a12.seq
12773 515_a12.seq
12813 cjb111_a12.seq
12813 h36b_a12.seq

FIGURE 19AB

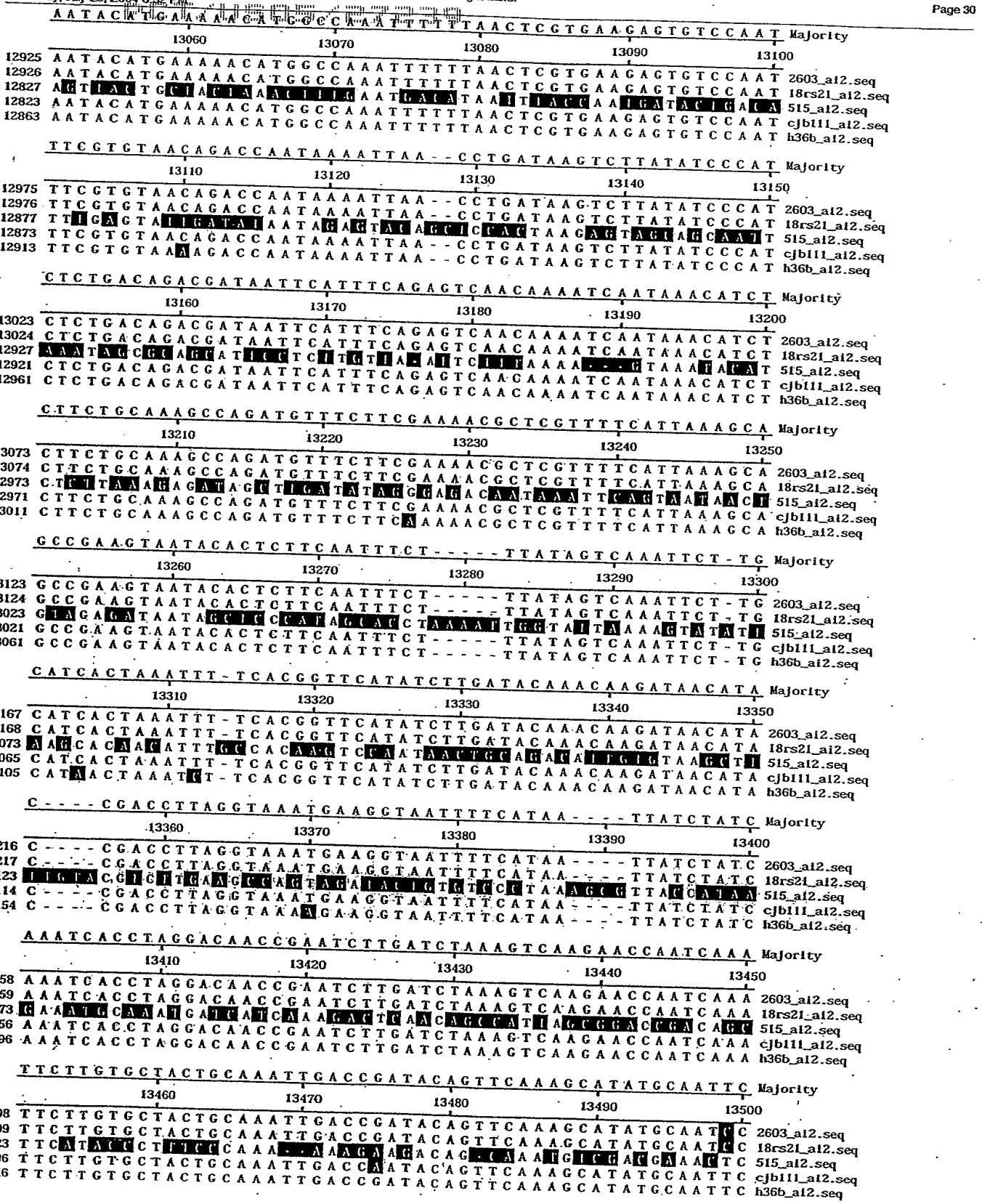

Majority
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq

FIGURE 19AC

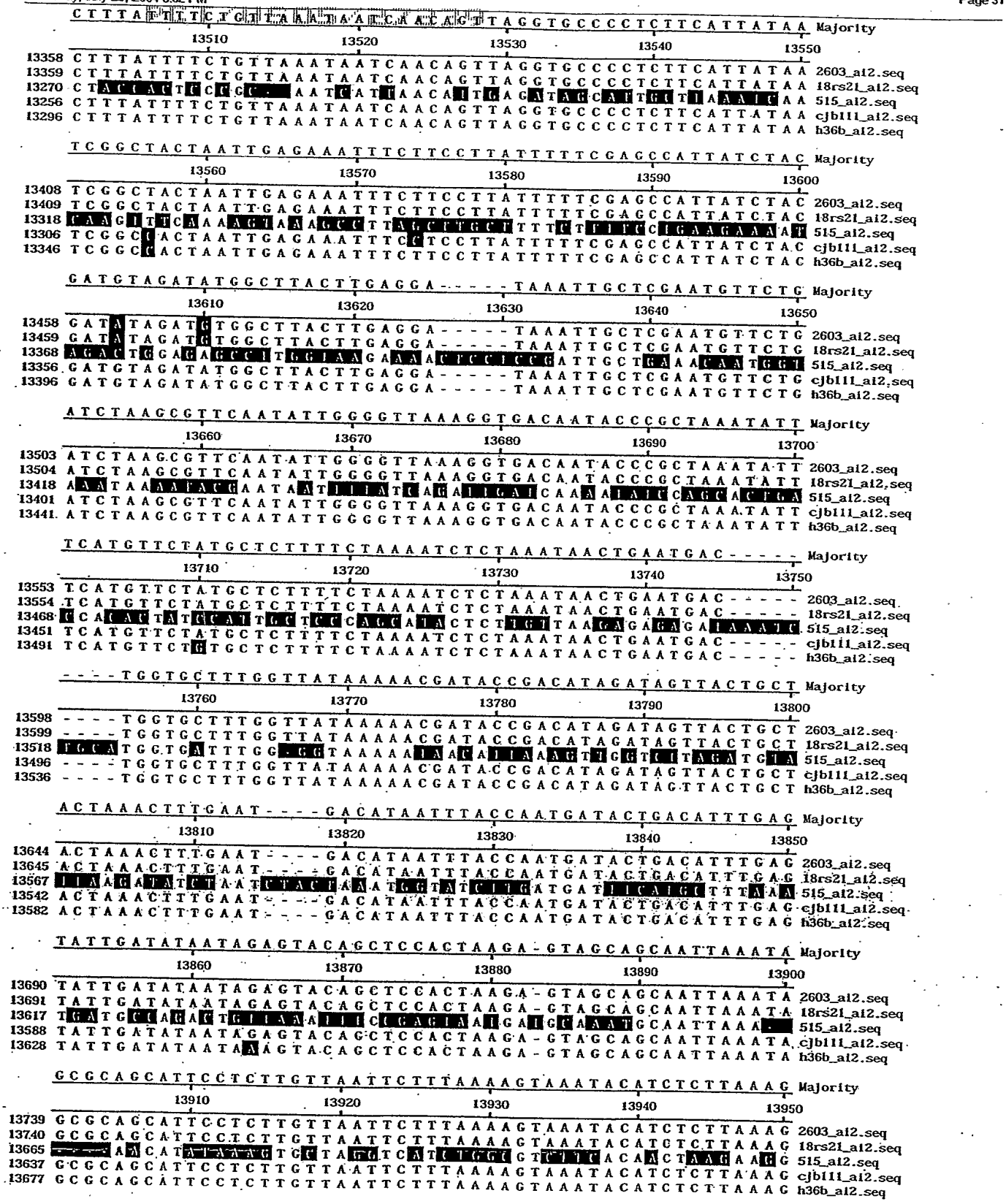
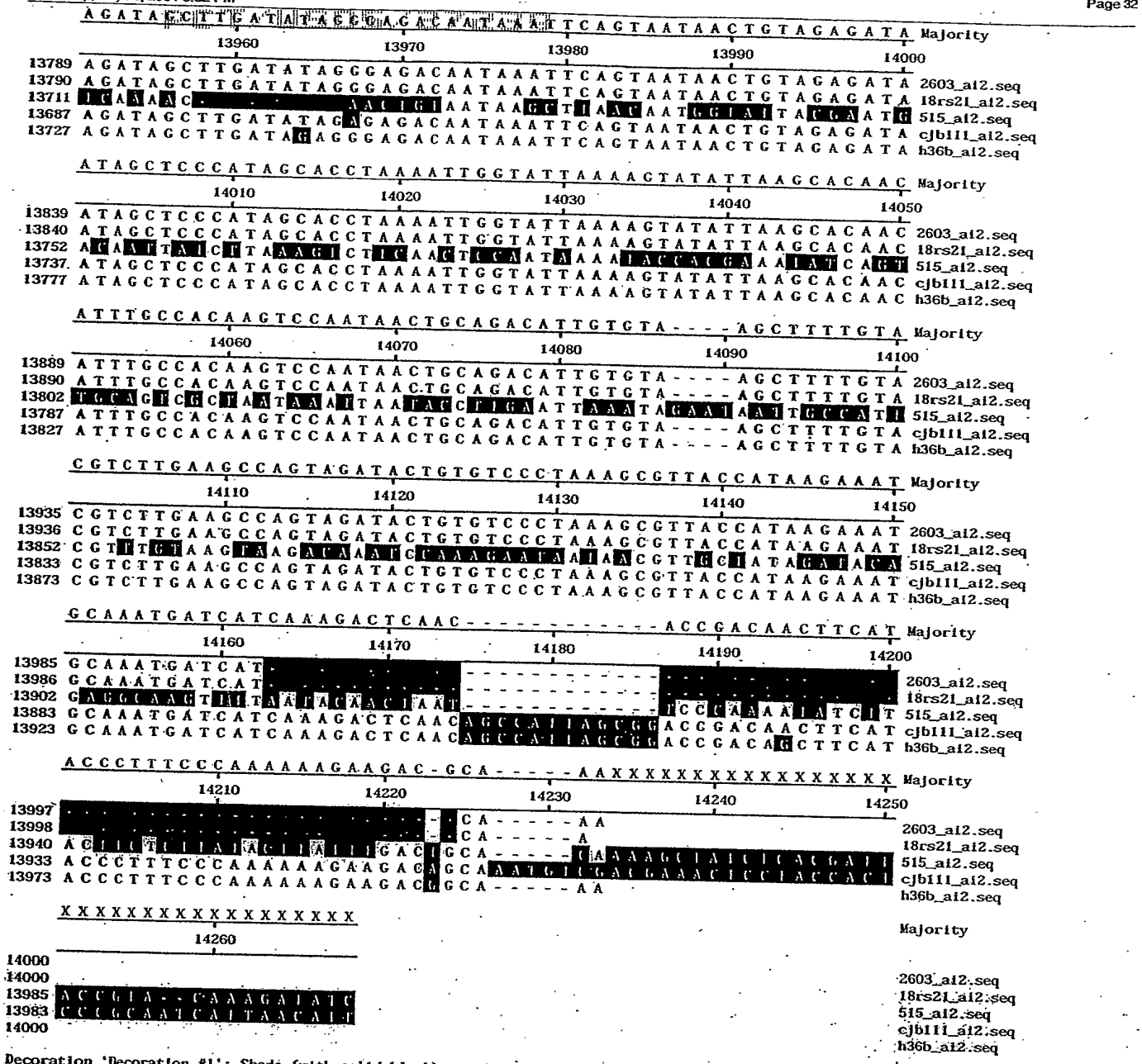

Majority
13510
13520
13530
13540
13550
2603_a12.seq
18rs21_a12.seq
515_a12.seq
cjb111_a12.seq
h36b_a12.seq
13560
13570
13580
13590
13600
13610
13620
13630
13640
13650
13660
13670
13680
13690
13700
13710
13720
13730
13740
13750
13760
13770
13780
13790
13800
13810
13820
13830
13840
13850
13860
13870
13880
13890
13900
13910
13920
13930
13940
13950

FIGURE 19AD



Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 19AE

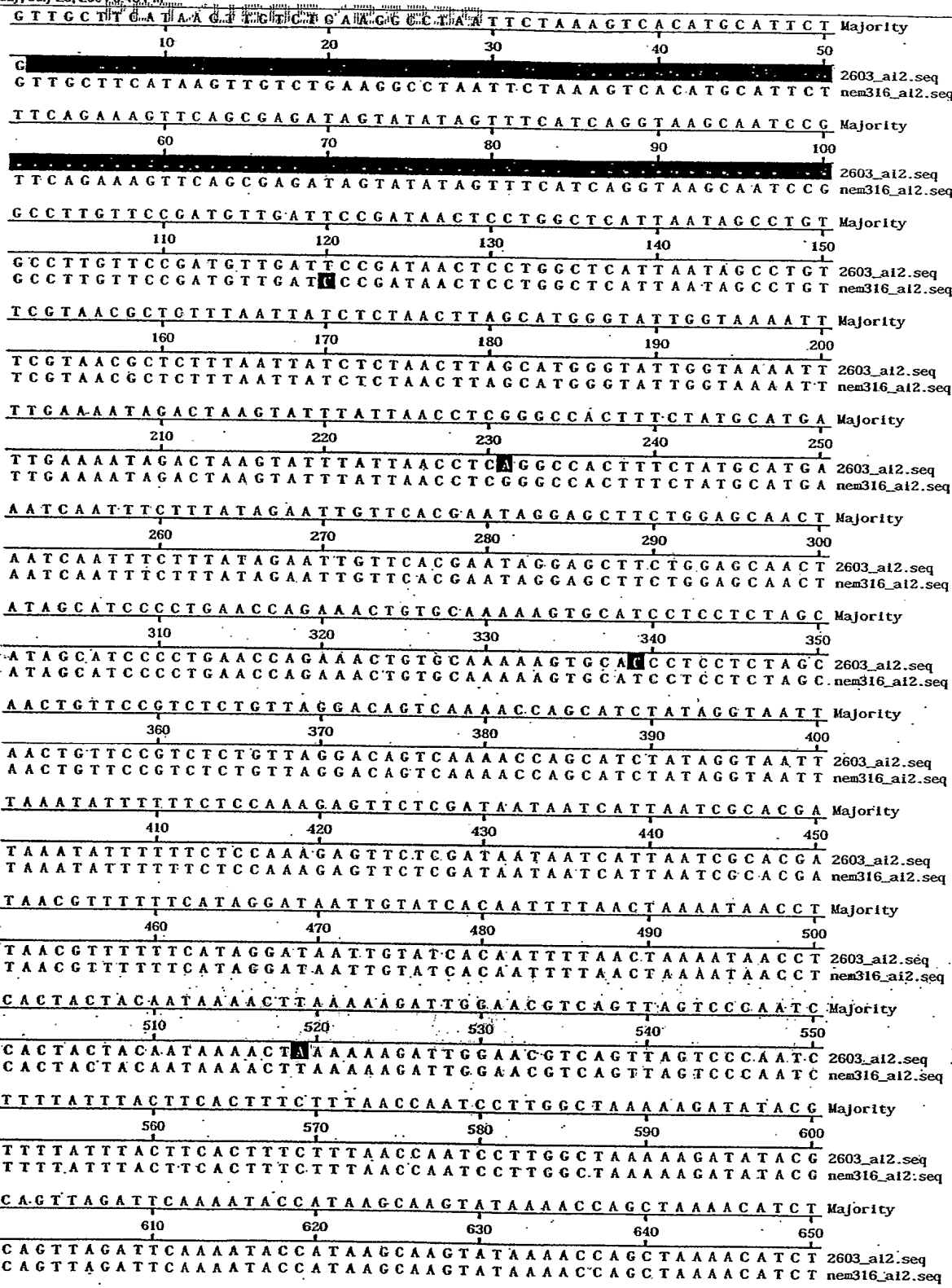

GTTGCTTCATAAGTTGTCTGAAGGCCTAATTCTAAAGTCACATGCATTCT Majority
10 20 30 40 50
1 G
1 GTTGCTTCATAAGTTGTCTGAAGGCCTAATTCTAAAGTCACATGCATTCT 2603_a12.seq
nem316_a12.seq
TTCAGAAAGTTCAGCGAGATAGTATATAGTTTCATCAGGTAAGCAATCCG Majority
60 70 80 90 100
2
51 TTCAGAAAGTTCAGCGAGATAGTATATAGTTTCATCAGGTAAGCAATCCG 2603_a12.seq
nem316_a12.seq
GCCTTGTTCCGATGTTGATTCCGATAACTCCTGGCTCATTAATAGCCTGT Majority
110 120 130 140 150
2 GCCTTGTTCCGATGTTGATTCCGATAACTCCTGGCTCATTAATAGCCTGT 2603_a12.seq
101 GCCTTGTTCCGATGTTGATCCCGATAACTCCTGGCTCATTAATAGCCTGT nem316_a12.seq
TCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAATT Majority
160 170 180 190 200
52 TCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAATT 2603_a12.seq
151 TCGTAACGCTCTTTAATTATCTCTAACTTAGCATGGGTATTGGTAAAATT nem316_a12.seq
TTGAAAATAGACTAAGTATTTATTAACCTCGGGCCACTTTCTATGCATGA Majority
210 220 230 240 250
102 TTGAAAATAGACTAAGTATTTATTAACCTCAGGCCACTTTCTATGCATGA 2603_a12.seq
201 TTGAAAATAGACTAAGTATTTATTAACCTCGGGCCACTTTCTATGCATGA nem316_a12.seq
AATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAACT Majority
260 270 280 290 300
152 AATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAACT 2603_a12.seq
251 AATCAATTTCTTTATAGAATTGTTCACGAATAGGAGCTTCTGGAGCAACT nem316_a12.seq
ATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCATCCTCCTCTAGC Majority
310 320 330 340 350
202 ATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCACCTCCTCTAGC 2603_a12.seq
301 ATAGCATCCCCTGAACCAGAAACTGTGCAAAAAGTGCATCCTCCTCTAGC nem316_a12.seq
AACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAATT Majority
360 370 380 390 400
252 AACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAATT 2603_a12.seq
351 AACTGTTCCGTCTCTGTTAGGACAGTCAAAACCAGCATCTATAGGTAATT nem316_a12.seq
TAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACGA Majority
410 420 430 440 450
302 TAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACGA 2603_a12.seq
401 TAAATATTTTTTCTCCAAAGAGTTCTCGATAATAATCATTAATCGCACGA nem316_a12.seq
TAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACCT Majority
460 470 480 490 500
352 TAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACCT 2603_a12.seq
451 TAACGTTTTTTCATAGGATAATTGTATCACAATTTTAACTAAAATAACCT nem316_a12.seq
CACTACTACAATAAAACTTAAAAAGATTGGAACGTCAGTTAGTCCCAATC Majority
510 520 530 540 550
402 CACTACTACAATAAAACTAAAAAAGATTGGAACGTCAGTTAGTCCCAATC 2603_a12.seq
501 CACTACTACAATAAAACTTAAAAAGATTGGAACGTCAGTTAGTCCCAATC nem316_a12.seq
TTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATACG Majority
560 570 580 590 600
452 TTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATACG 2603_a12.seq
551 TTTTATTTACTTCACTTTCTTTAACCAATCCTTGGCTAAAAAGATATACG nem316_a12.seq
CAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATCT Majority
610 620 630 640 650
502 CAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATCT 2603_a12.seq
601 CAGTTAGATTCAAAATACCATAAGCAAGTATAAAACCAGCTAAAACATCT nem316_a12.seq

Figure 20

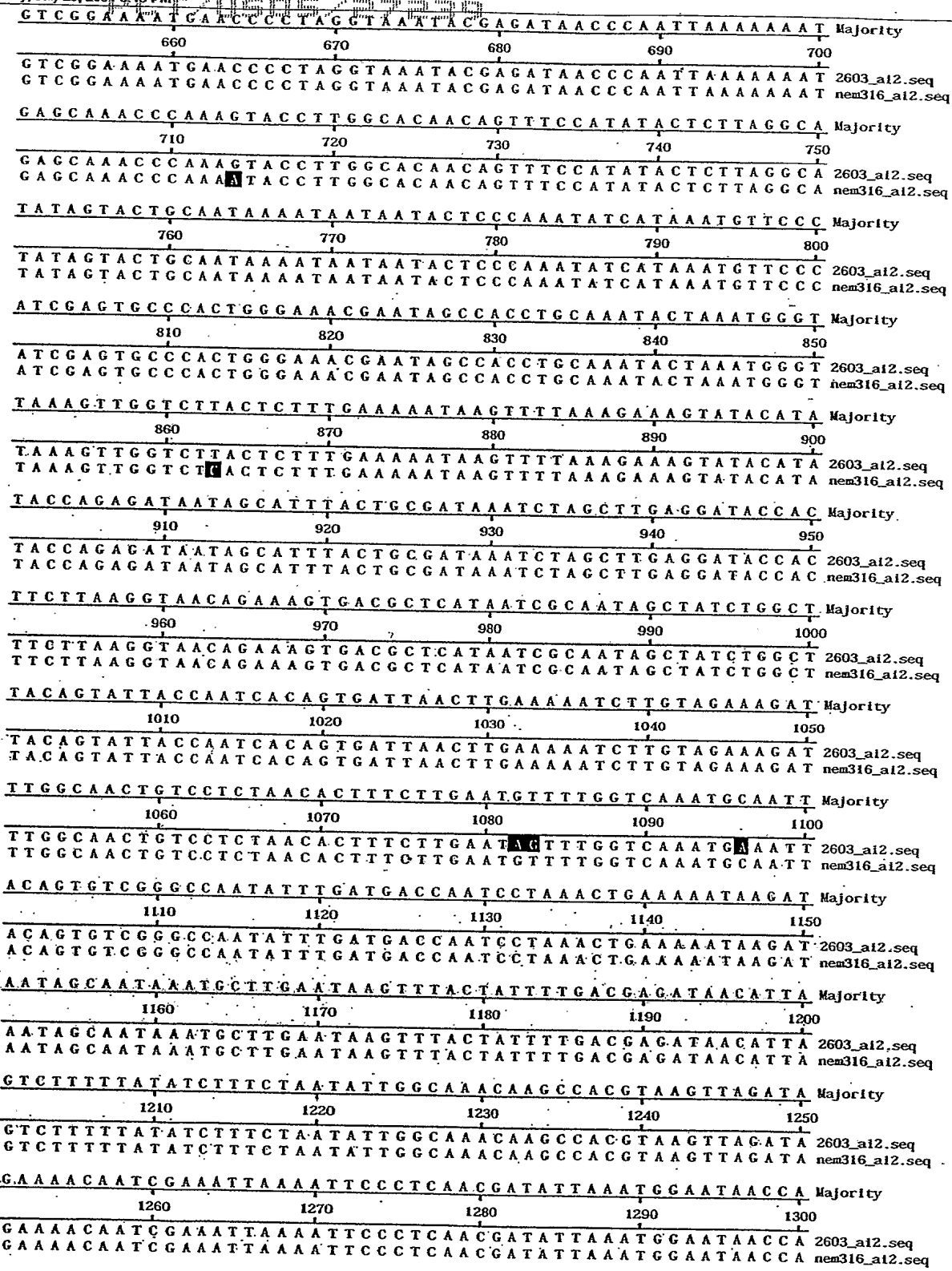

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FIGURE 20A

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FIGURE 20B

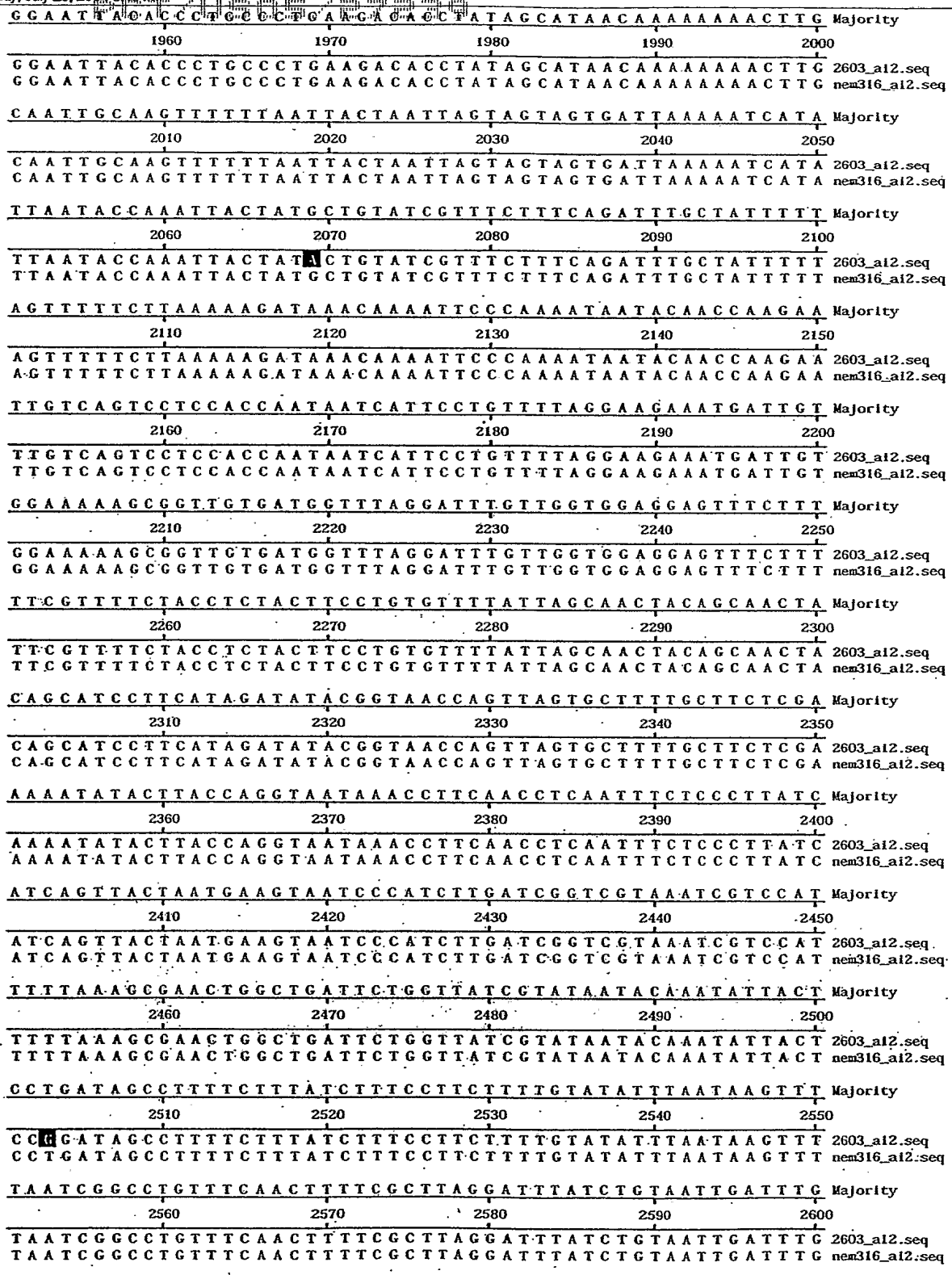
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FIGURE 20C

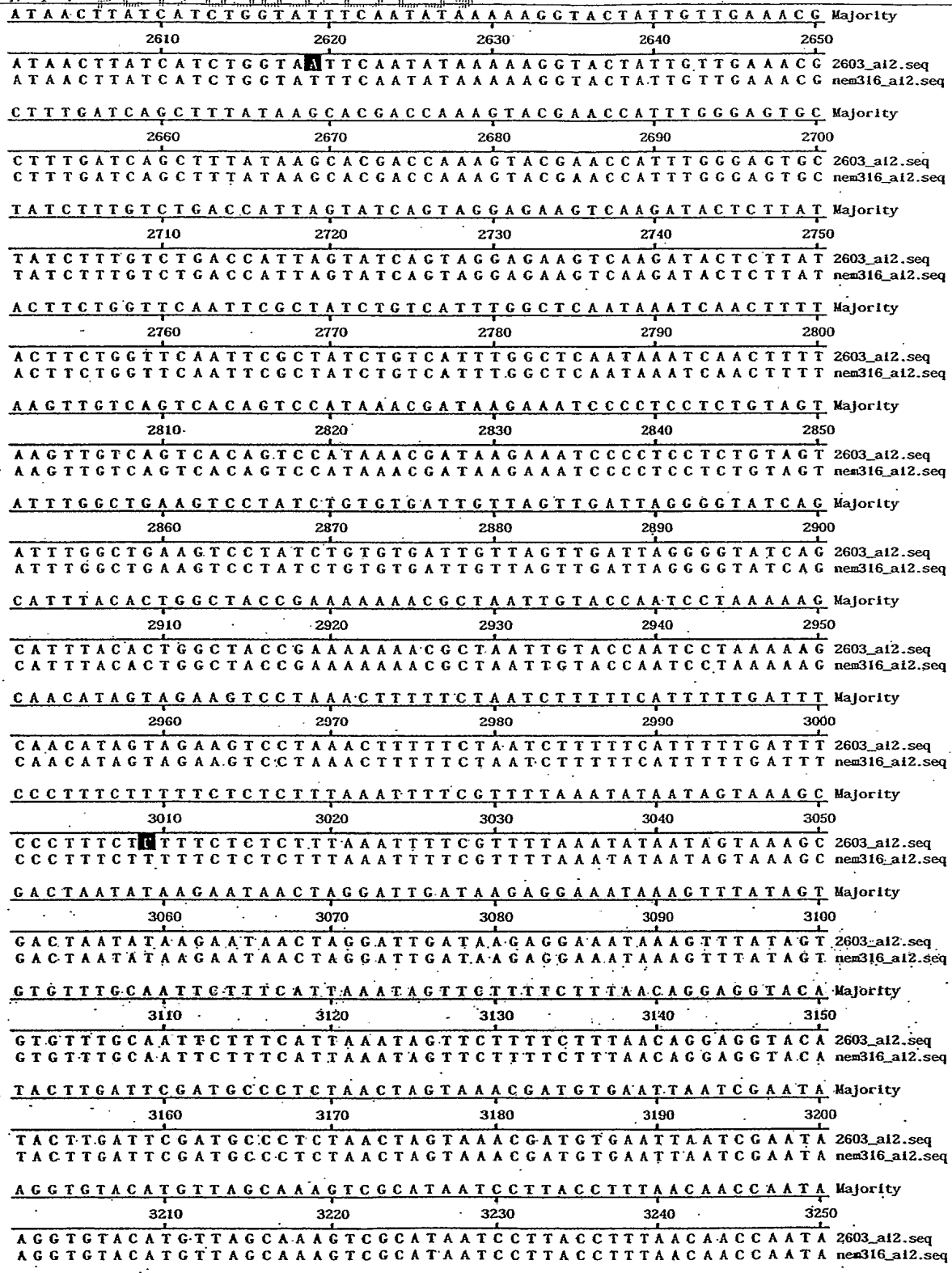
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FIGURE 20D

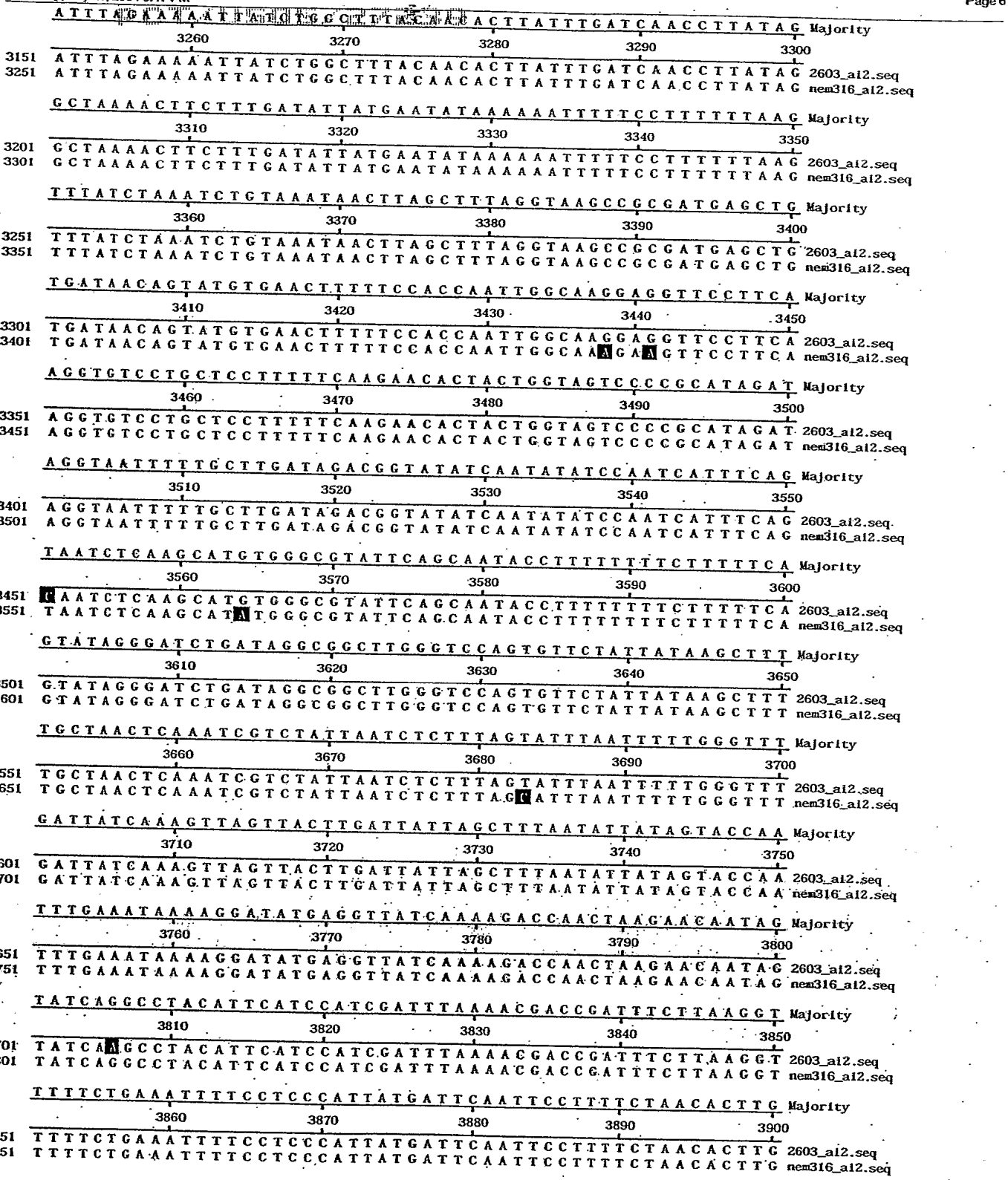
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FIGURE 20E

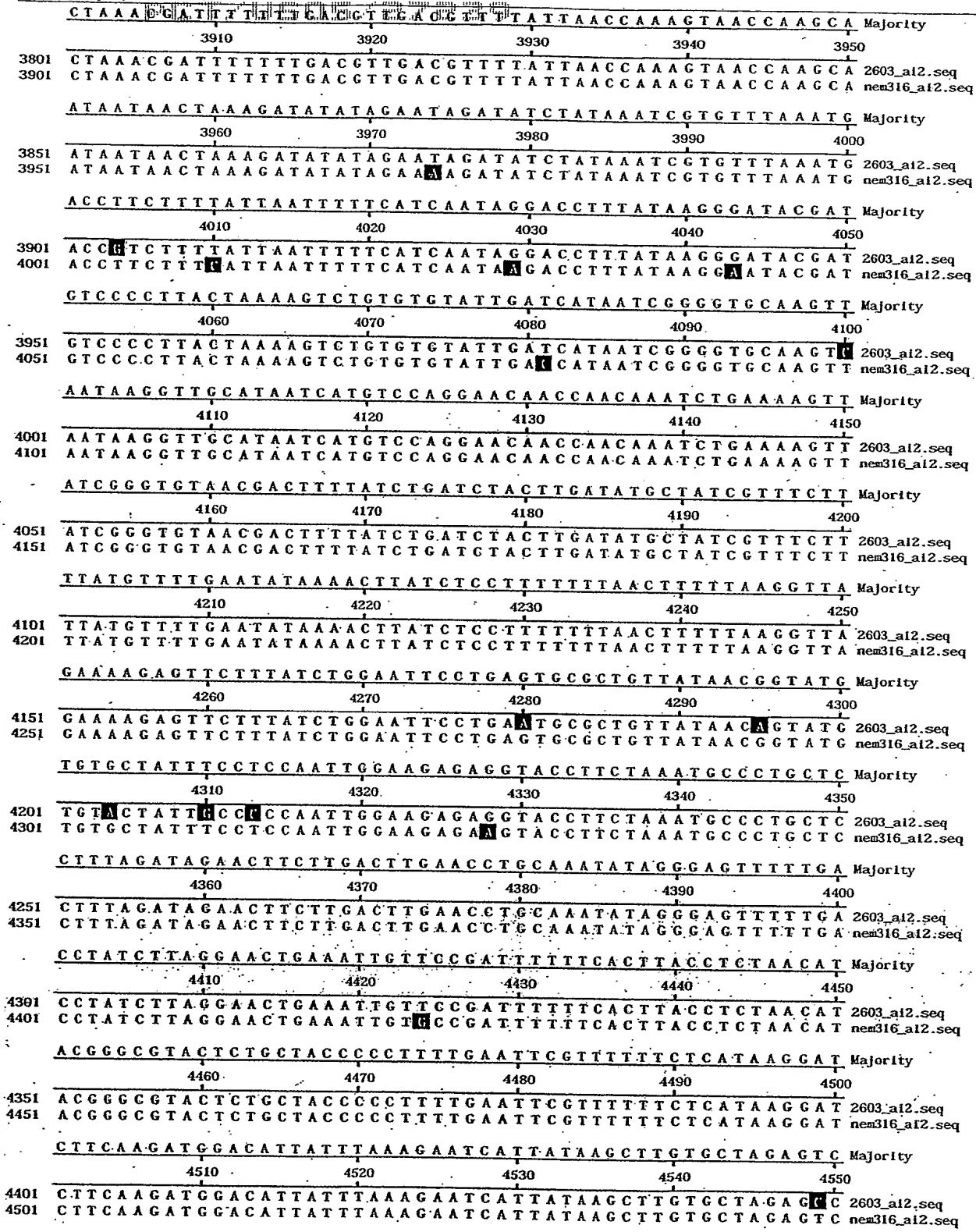
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FIGURE 20F

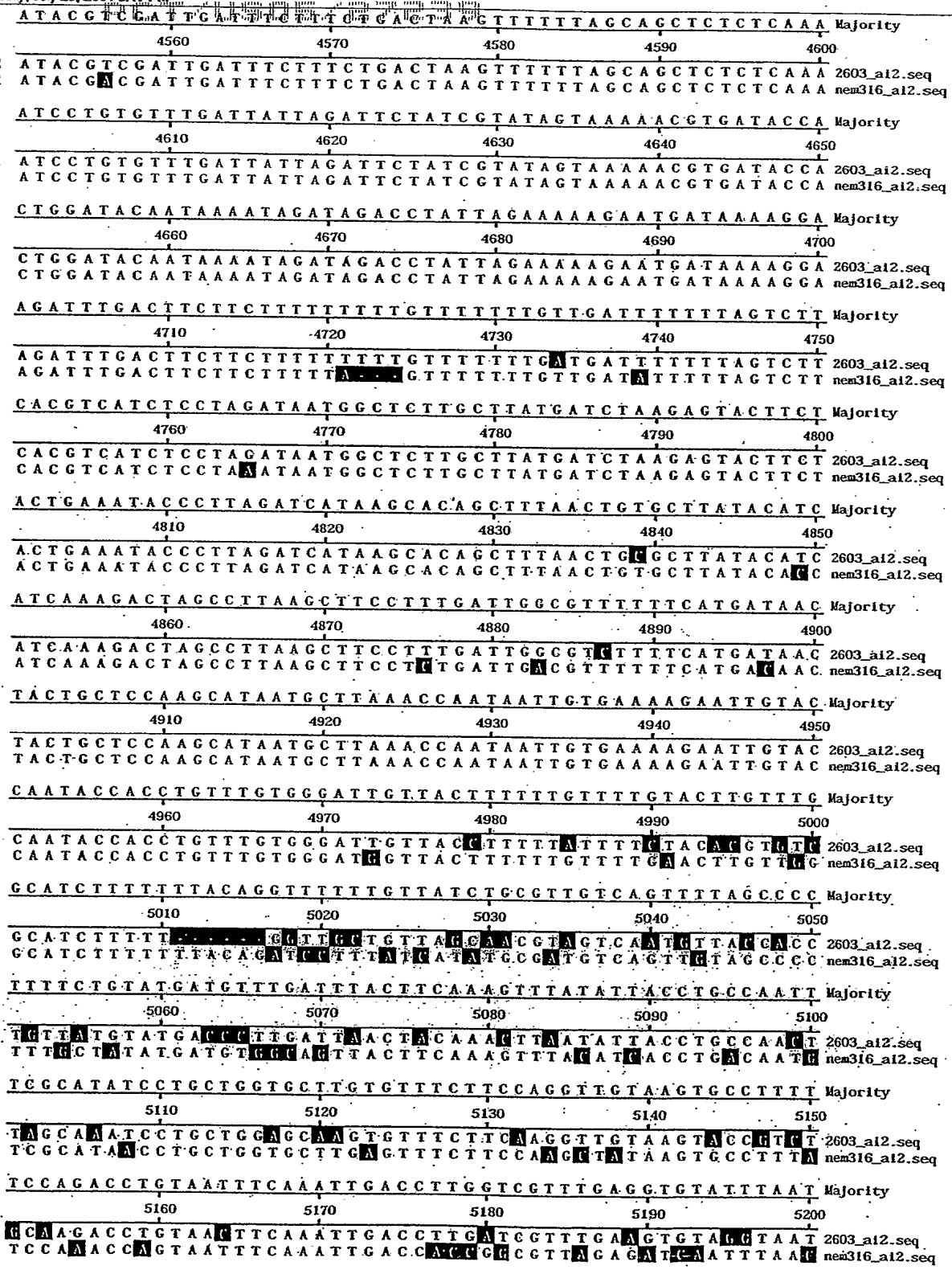
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FIGURE 20G

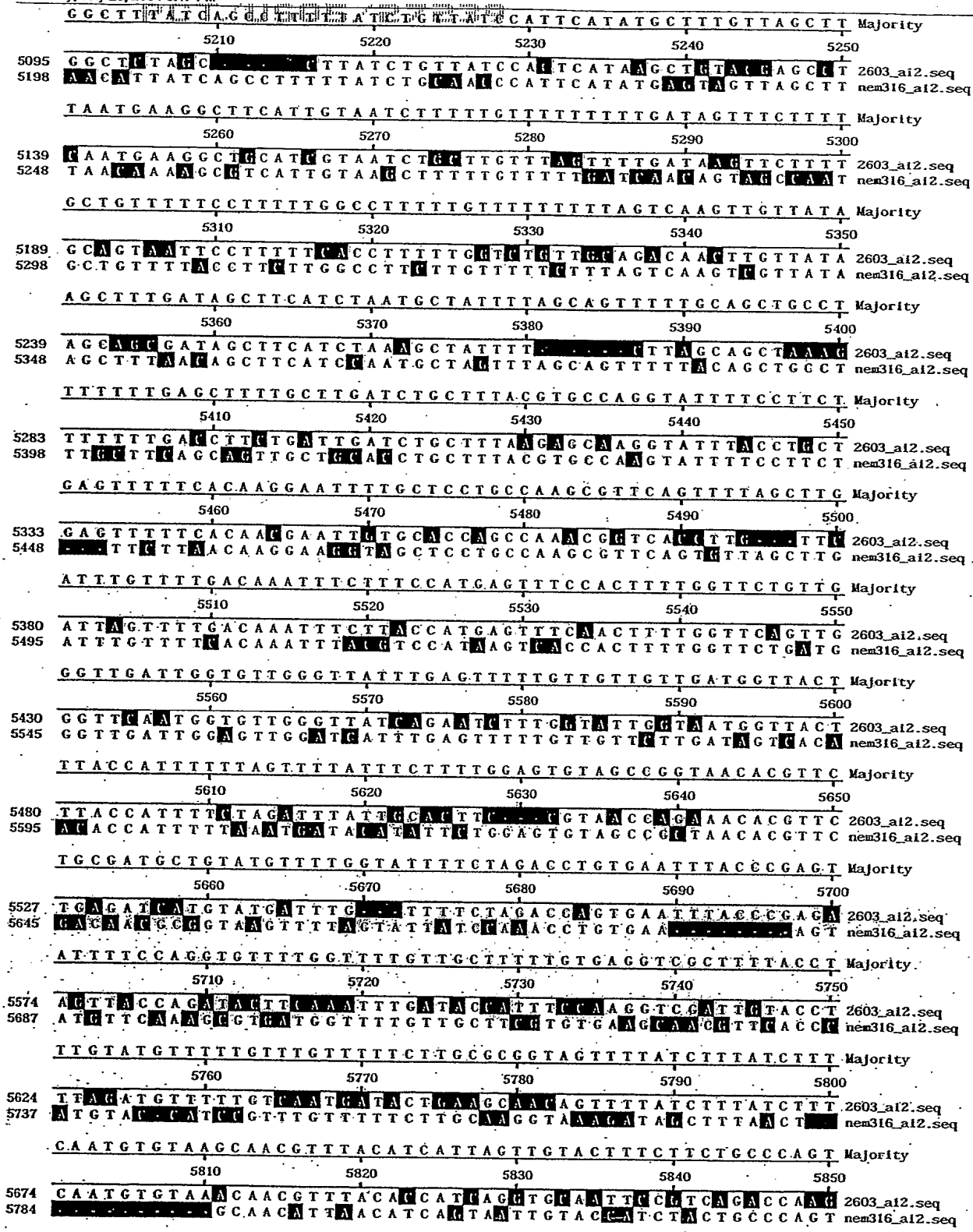


FIGURE 20H

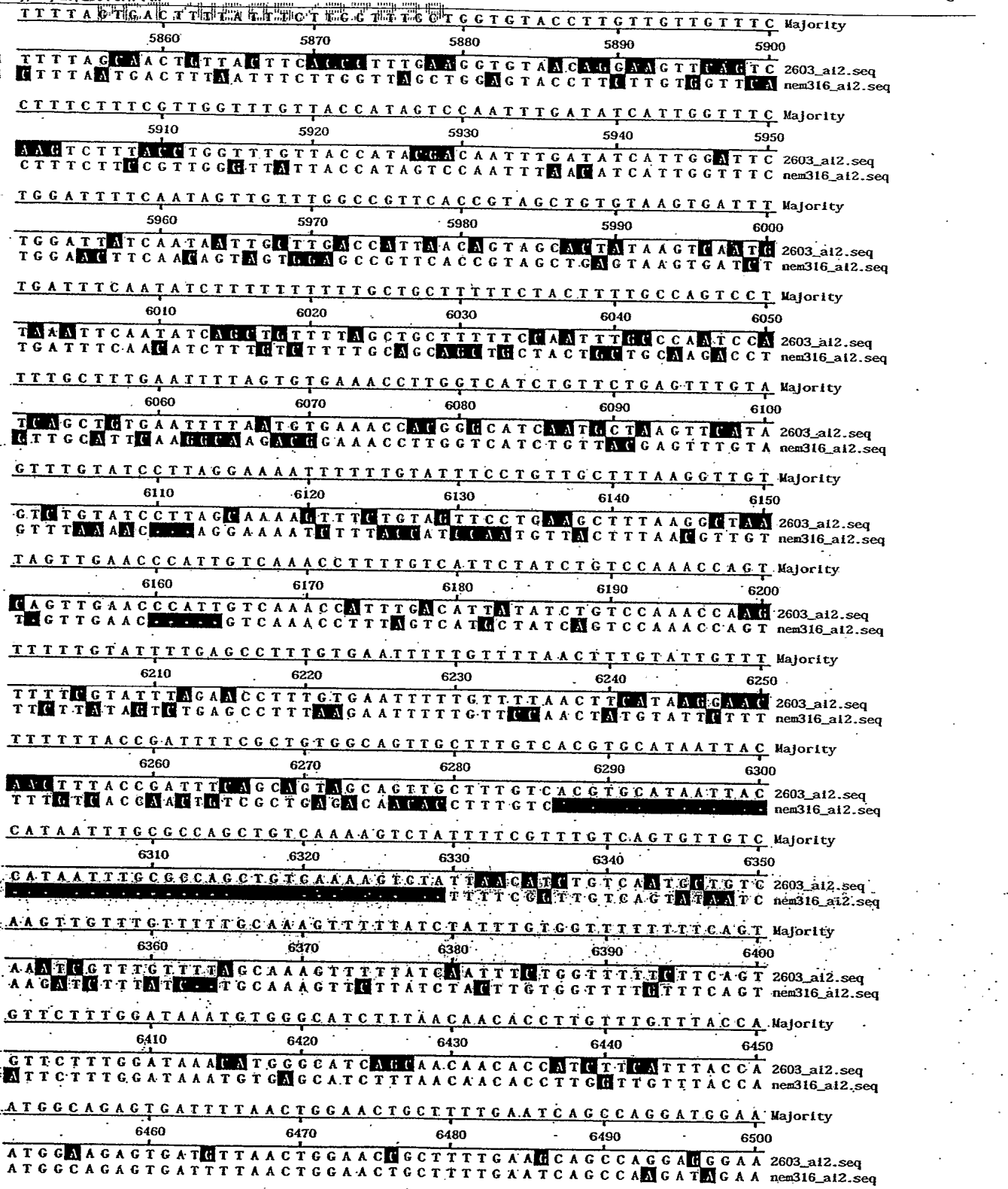
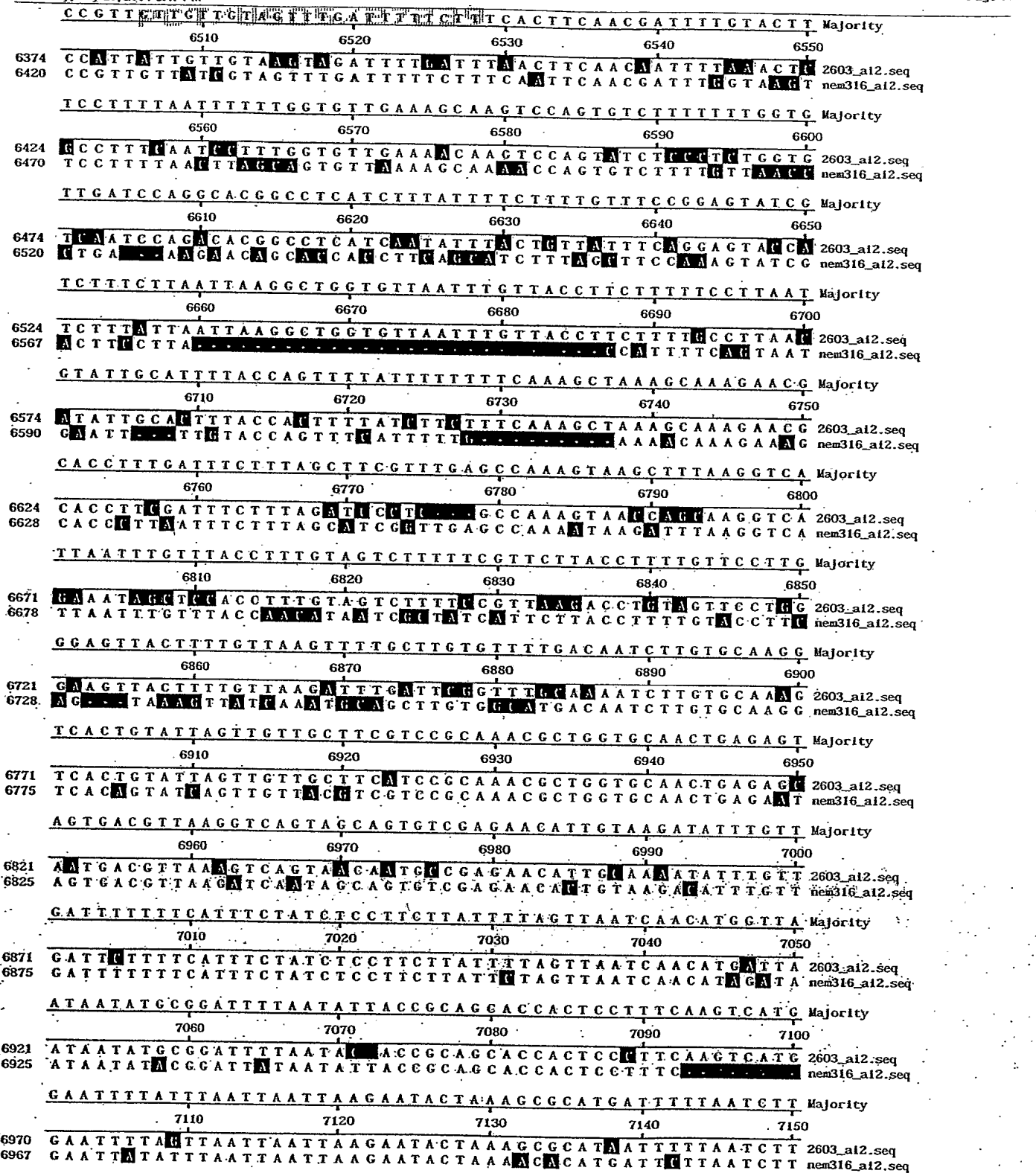


FIGURE 20I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Majority
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6474 2603_a12.seq
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Majority
6660 6670 6680 6690 6700
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Majority
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6574 2603_a12.seq
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Majority
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Majority
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6771 2603_a12.seq
6775 nem316_a12.seq
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6871 2603_a12.seq
6875 nem316_a12.seq
Majority
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6921 2603_a12.seq
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Majority
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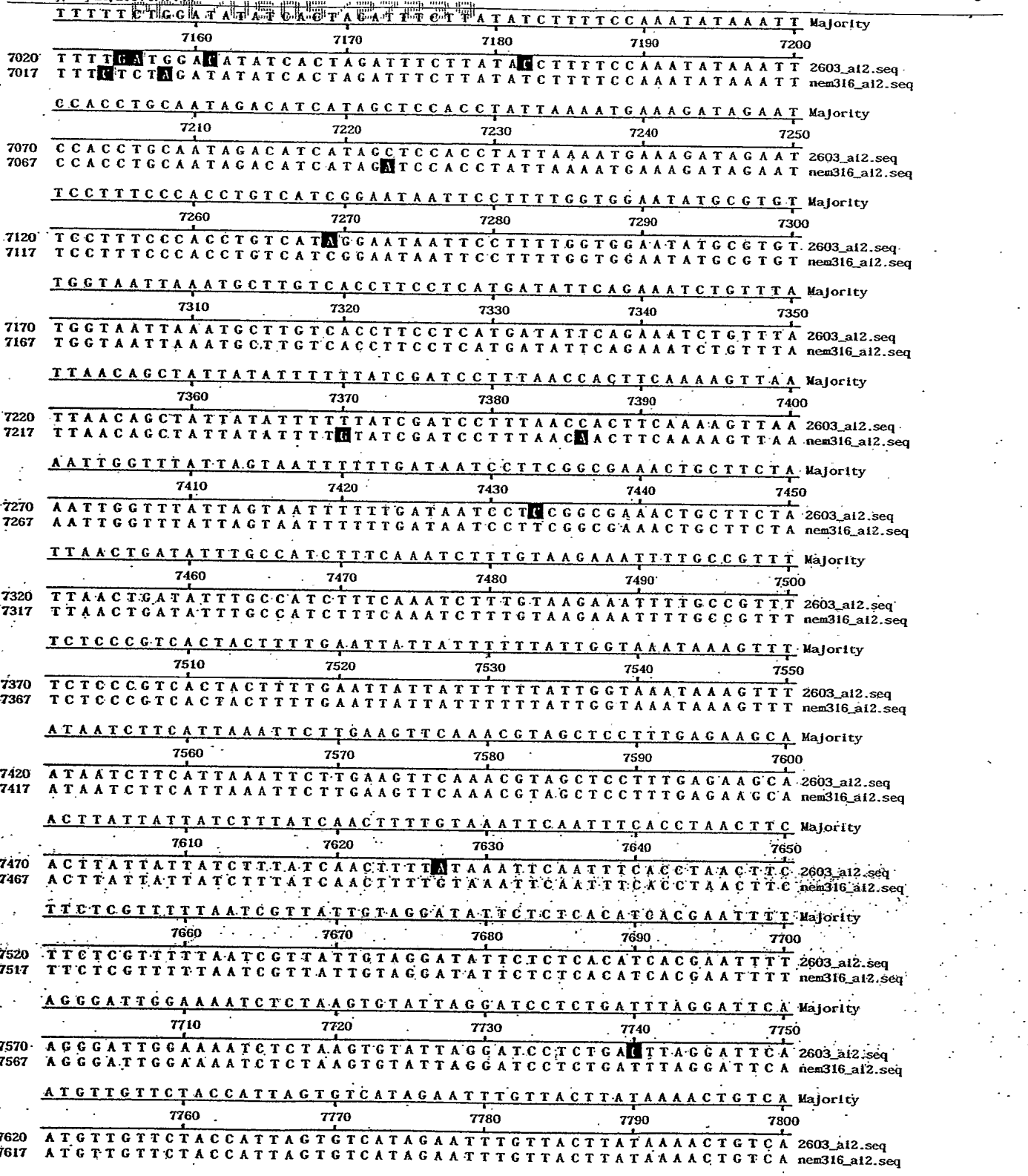
6967 nem316_a12.seq

FIGURE 20J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7070 CCACCTGCAATAGACATCATAGCTCCACCTATTAAAATGAAAGATAGAAT 2603_al2.seq
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7617 ATGTTGTTCTACCATTAGTGTCATAGAATTTGTTACTTATAAAACTGTCA nem316_al2.seq

FIGURE 20K

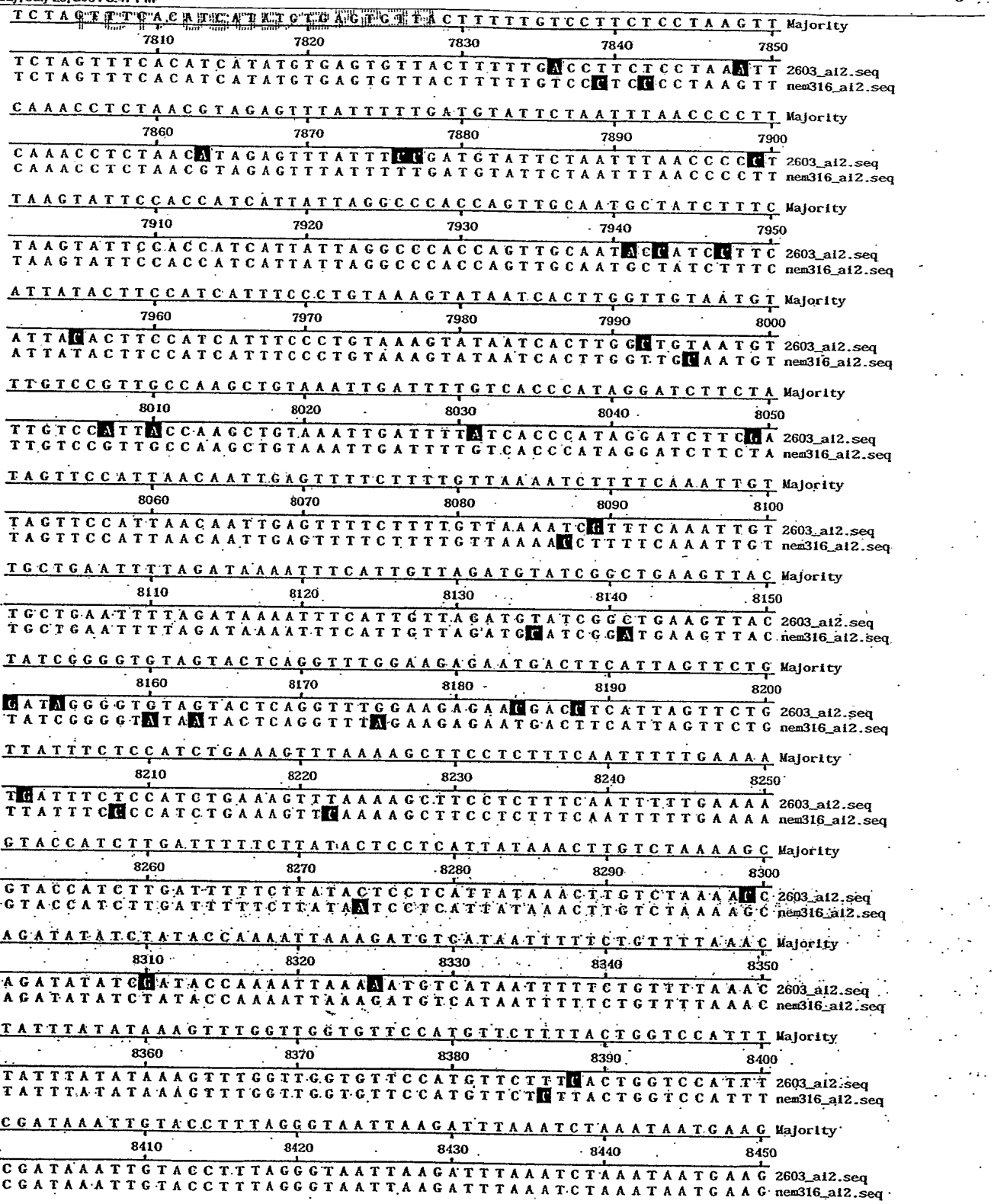

FIGURE 20L

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8367  ACAAAAAGTAACTCTCCCCATTTCCTTTTATATCCTCGGGCTTATCAGTA nem316_al2.seq

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8517  TTGTTGGAACACCATCAGTTATATGAACAATAATTTTTTGACTATTTCGA nem316_al2.seq

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FIGURE 20M

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                        9360      9370      9380      9390      9400
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FIGURE 20N

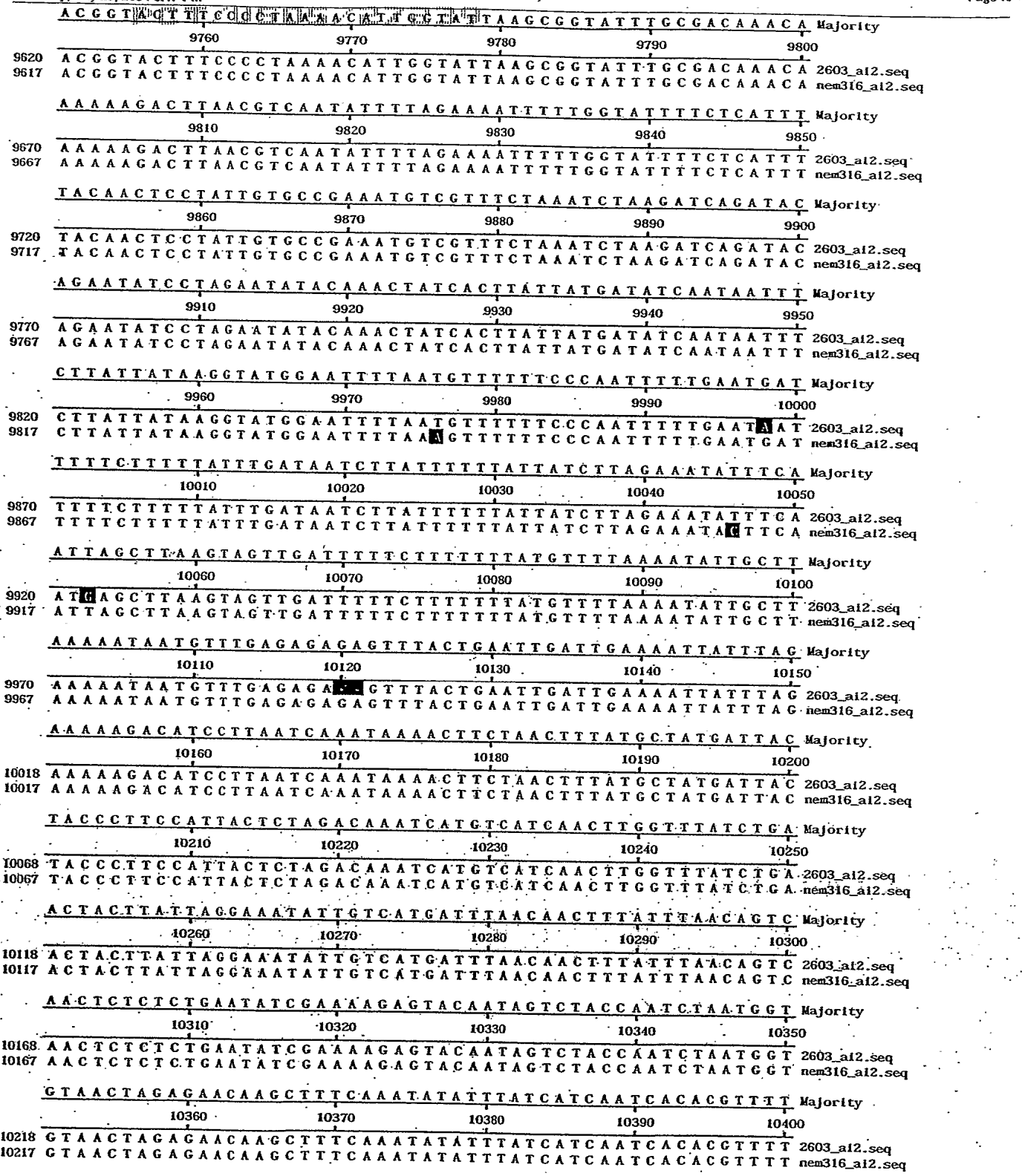
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FIGURE 20O

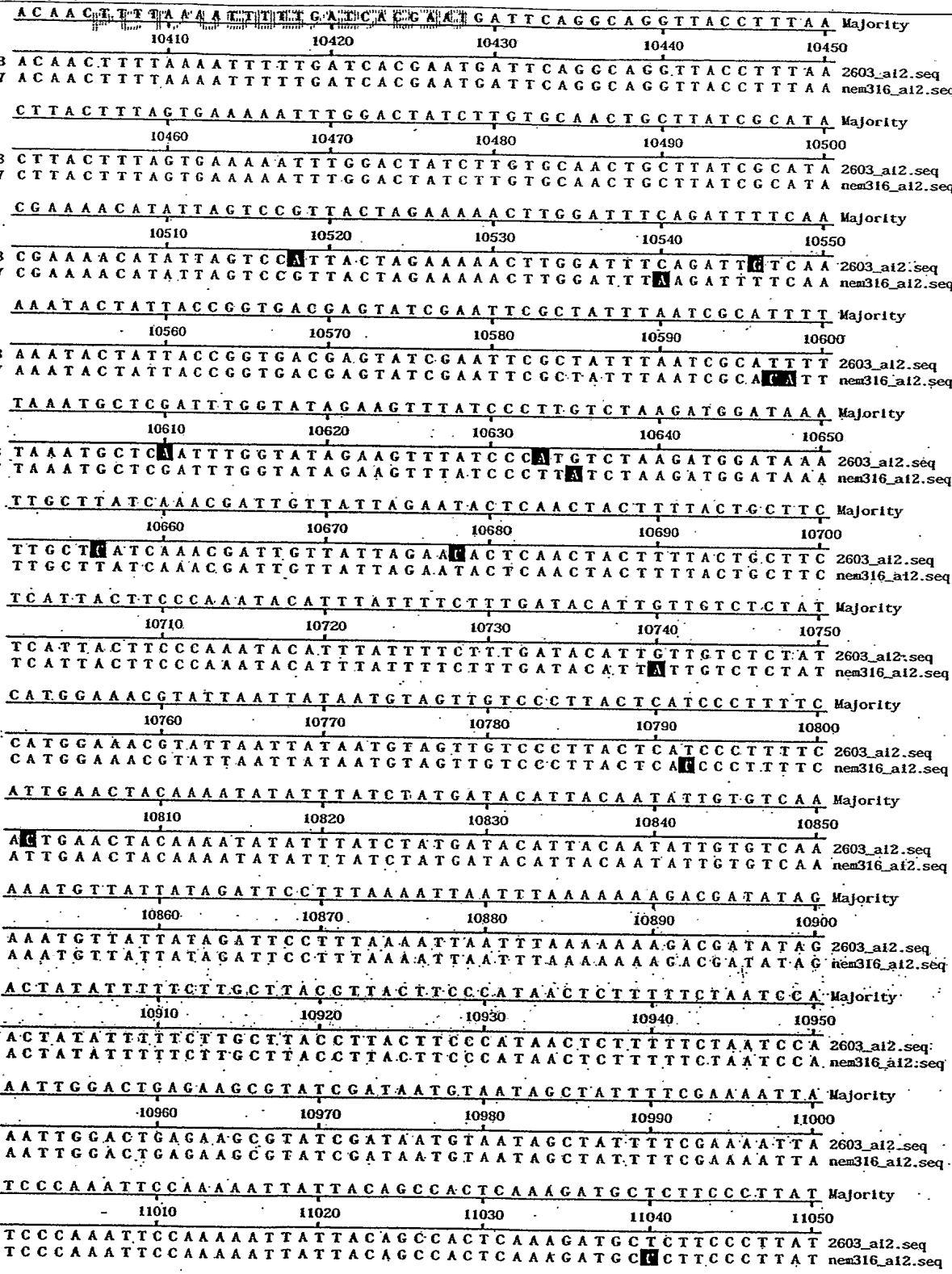
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FIGURE 20P

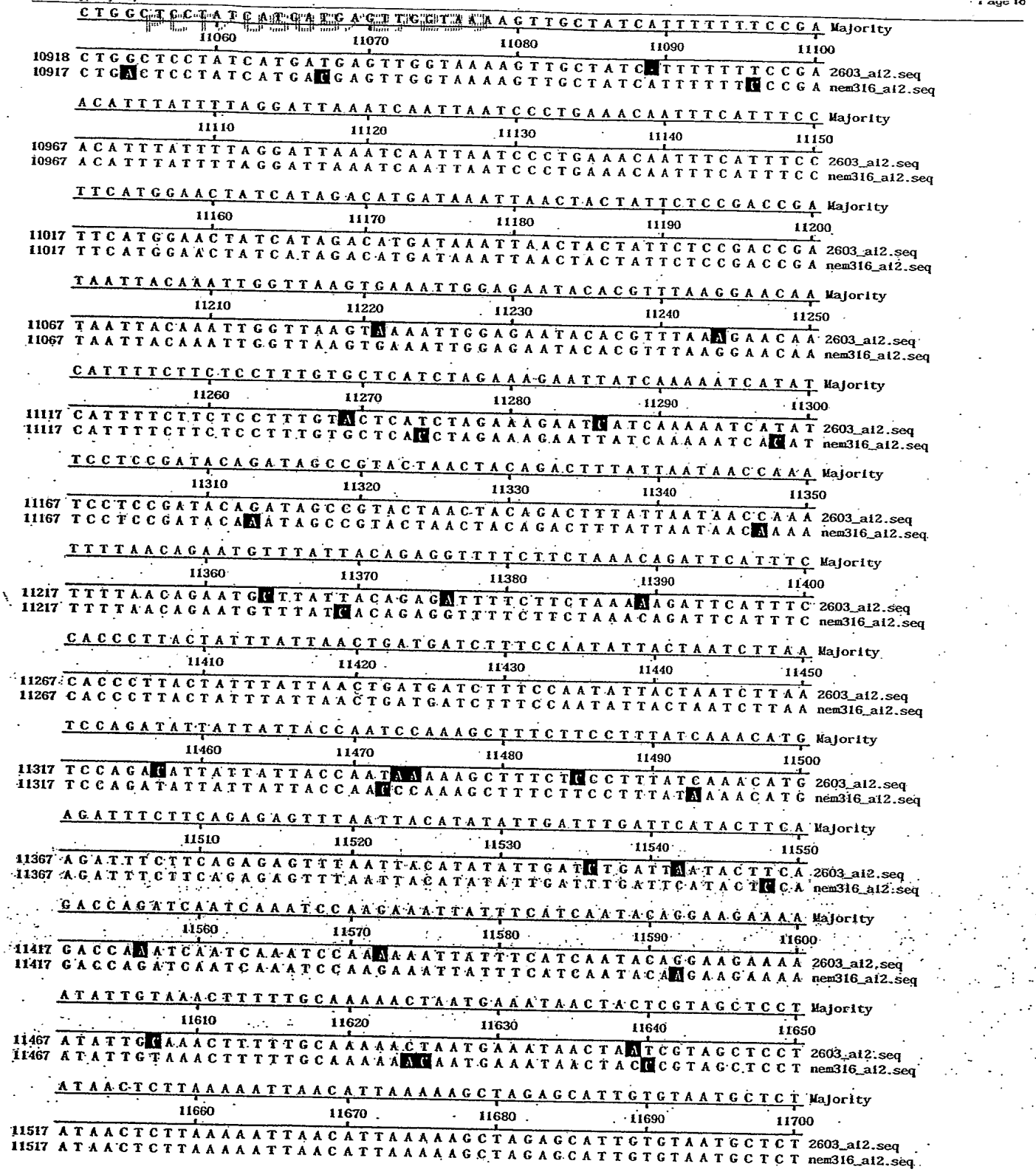
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FIGURE 20Q

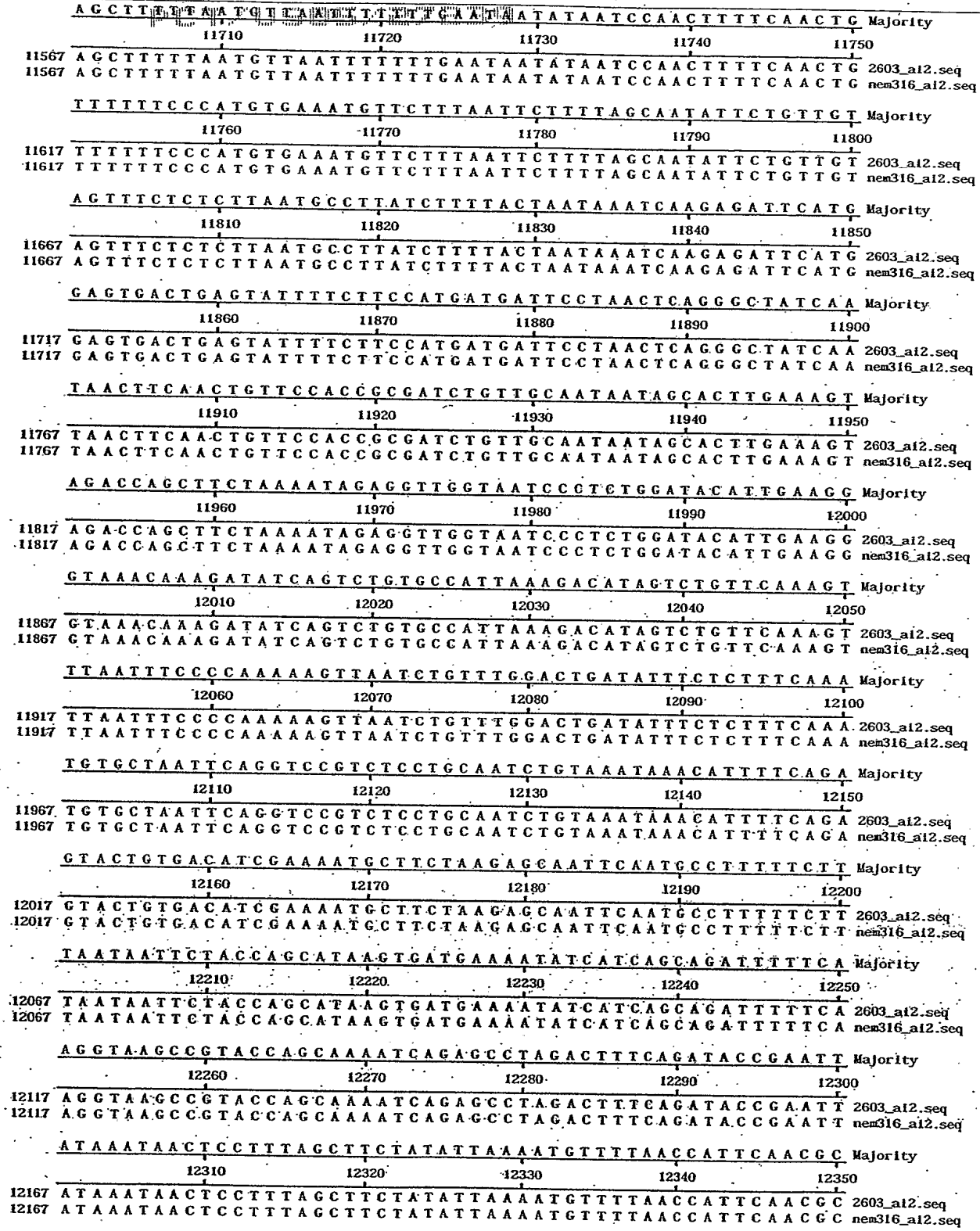
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FIGURE 20R

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FIGURE 20S

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CGACCTTAGGTAAATGAAGGTAATTTTCATAATTATCTATCAAATCACCT Majority
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13217 CGACCTTAGGTAAATGAAGGTAATTTTCATAATTATCTATCAAATCACCT 2603_a12.seq
13217 CGACCTTAGGTAAATGAAGGTAATTTTCATAATTATCTATCAAATCACCT nem316_a12.seq

AGGACAACCGAATCTTGATCTAAAGTCAAGAACCAATCAAATTCTTGTGC Majority
          13410     13420     13430     13440     13450
13267 AGGACAACCGAATCTTGATCTAAAGTCAAGAACCAATCAAATTCTTGTGC 2603_a12.seq
13267 AGGACAACCGAATCTTGATCTAAAGTCAAGAACCAATCAAATTCTTGTGC nem316_a12.seq

TACTGCAAATTGACCGATACAGTTCAAAGCATATGCAATCCCTTTATTTT Majority
          13460     13470     13480     13490     13500
13317 TACTGCAAATTGACCGATACAGTTCAAAGCATATGCAATCCCTTTATTTT 2603_a12.seq
13317 TACTGCAAATTGACCGATACAGTTCAAAGCATATGCAATCCCTTTATTTT nem316_a12.seq

CTGTTAAATAATCAACAGTTAGGTGCCCCTCTTCATTATAATCGGCTACT Majority
          13510     13520     13530     13540     13550
13367 CTGTTAAATAATCAACAGTTAGGTGCCCCTCTTCATTATAATCGGCTACT 2603_a12.seq
13367 CTGTTAAATAATCAACAGTTAGGTGCCCCTCTTCATTATAATCGGCTACT nem316_a12.seq

AATTGAGAAATTTCTTCCTTATTTTTCGAGCCATTATCTACGATATAGAT Majority
          13560     13570     13580     13590     13600
13417 AATTGAGAAATTTCTTCCTTATTTTTCGAGCCATTATCTACGATATAGAT 2603_a12.seq
13417 AATTGAGAAATTTCTTCCTTATTTTTCGAGCCATTATCTACGATATAGAT nem316_a12.seq

GTGGCTTACTTGAGGATAAATTGCTCGAATGTTCTGATCTAAGCGTTCAA Majority
          13610     13620     13630     13640     13650
13467 GTGGCTTACTTGAGGATAAATTGCTCGAATGTTCTGATCTAAGCGTTCAA 2603_a12.seq
13467 GTGGCTTACTTGAGGATAAATTGCTCGAATGTTCTGATCTAAGCGTTCAA nem316_a12.seq
```

FIGURE 20T

```
TATTGGGGTTAAAGGTGACAATACCCGCTAAATATTTCATGTTCTATGCT Majority
PCT/US2005/027239
13660 13670 13680 13690 13700
13517 TATTGGGGTTAAAGGTGACAATACCCGCTAAATATTTCATGTTCTATGCT 2603_a12.seq
13517 TATTGGGGTTAAAGGTGACAATACCCGCTAAATATTTCATGTTCTATGCT nem316_a12.seq

CTTTTCTAAAATCTCTAAATAACTGAATGACTGGTGCTTTGGTTATAAAA Majority
13710 13720 13730 13740 13750
13567 CTTTTCTAAAATCTCTAAATAACTGAATGACTGGTGCTTTGGTTATAAAA 2603_a12.seq
13567 CTTTTCTAAAATCTCTAAATAACTGAATGACTGGTGCTTTGGTTATAAAA nem316_a12.seq

ACGATACCGACATAGATAGTTACTGCTACTAAACTTTGAATGACATAATT Majority
13760 13770 13780 13790 13800
13617 ACGATACCGACATAGATAGTTACTGCTACTAAACTTTGAATGACATAATT 2603_a12.seq
13617 ACGATACCGACATAGATAGTTACTGCTACTAAACTTTGAATGACATAATT nem316_a12.seq

TACCAATGATACTGACATTTGAGTATTGATATAATAGAGTACAGCTCCAC Majority
13810 13820 13830 13840 13850
13667 TACCAATGATACTGACATTTGAGTATTGATATAATAGAGTACAGCTCCAC 2603_a12.seq
13667 TACCAATGATACTGACATTTGAGTATTGATATAATAGAGTACAGCTCCAC nem316_a12.seq

TAAGAGTAGCAGCAATTAAATAGCGCAGCATTCCTCTTGTTAATTCTTTA Majority
13860 13870 13880 13890 13900
13717 TAAGAGTAGCAGCAATTAAATAGCGCAGCATTCCTCTTGTTAATTCTTTA 2603_a12.seq
13717 TAAGAGTAGCAGCAATTAAATAGCGCAGCATTCCTCTTGTTAATTCTTTA nem316_a12.seq

AAAGTAAATACATCTCTTAAAGAGATAGCTTGATATAGGGAGACAATAAA Majority
13910 13920 13930 13940 13950
13767 AAAGTAAATACATCTCTTAAAGAGATAGCTTGATATAGGGAGACAATAAA 2603_a12.seq
13767 AAAGTAAATACATCTCTTAAAGAGATAGCTTGATATAGGGAGACAATAAA nem316_a12.seq

TTCAGTAATAACTGTAGAGATAATAGCTCCCATAGCACCTAAAATTGGTA Majority
13960 13970 13980 13990 14000
13817 TTCAGTAATAACTGTAGAGATAATAGCTCCCATAGCACCTAAAATTGGTA 2603_a12.seq
13817 TTCAGTAATAACTGTAGAGATAATAGCTCCCATAGCACCTAAAATTGGTA nem316_a12.seq

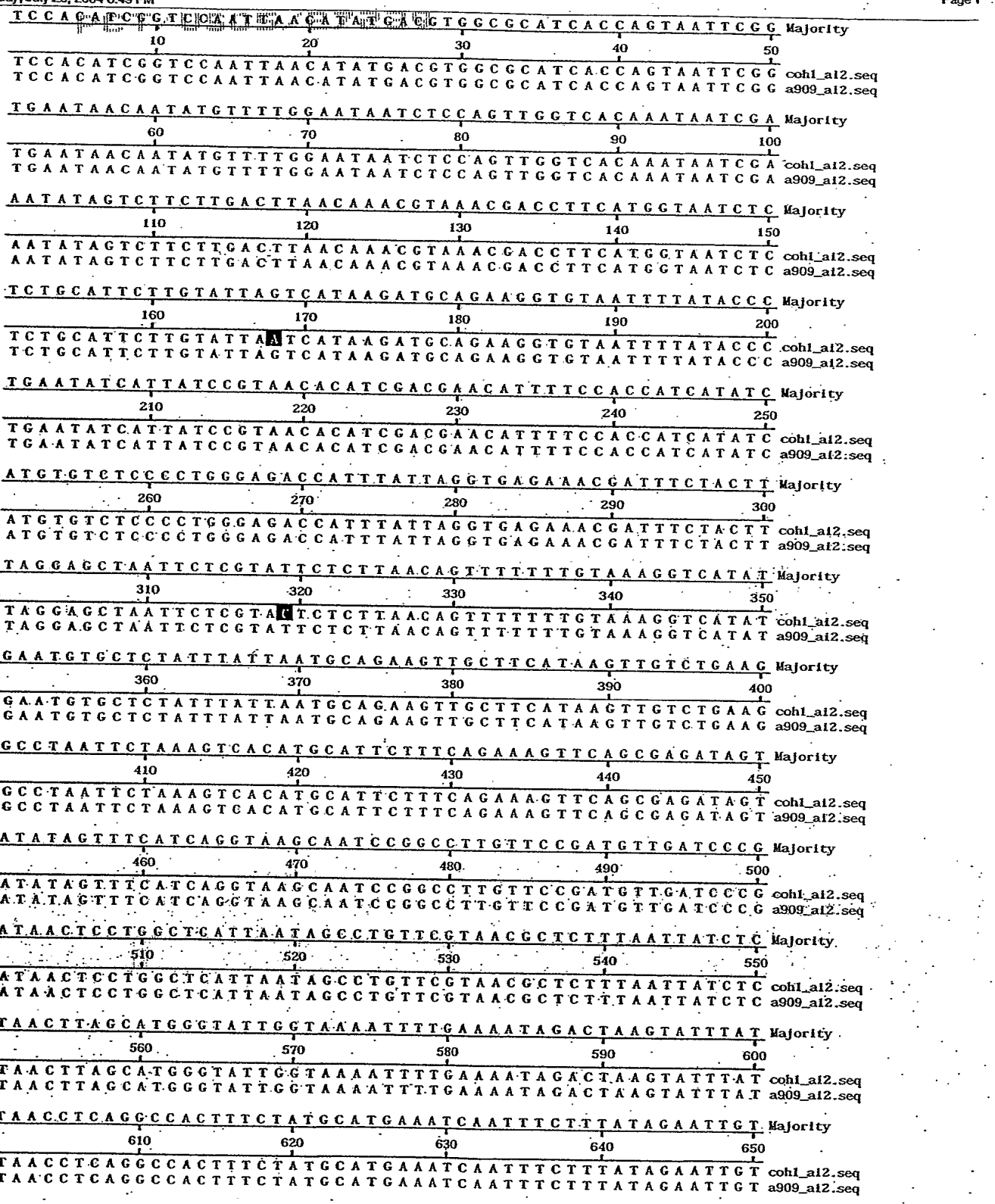
TTAAAAGTATATTAAGCACAACATTTGCCACAAGTCCAATAACTGCAGAC Majority
14010 14020 14030 14040 14050
13867 TTAAAAGTATATTAAGCACAACATTTGCCACAAGTCCAATAACTGCAGAC 2603_a12.seq
13867 TTAAAAGTATATTAAGCACAACATTTGCCACAAGTCCAATAACTGCAGAC nem316_a12.seq

ATTGTGTAAGCTTTTGTACGTCTTGAAGCCAGTAGATACTGTGTCCCTAA Majority
14060 14070 14080 14090 14100
13917 ATTGTGTAAGCTTTTGTACGTCTTGAAGCCAGTAGATACTGTGTCCCTAA 2603_a12.seq
13917 ATTGTGTAAGCTTTTGTACGTCTTGAAGCCAGTAGATACTGTGTCCCTAA nem316_a12.seq

AGCGTTACCATAAGAAATGCAAATGATCATCAAA Majority
14110 14120 14130
13967 AGCGTTACCATAAGAAATGCAAATGATCATCAAA 2603_a12.seq
13967 AGCGTTACCATAAGAAATGCAAATGATCATCAAA nem316_a12.seq
```

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 20U


TCCACATCGGTCCAATTAACATATGACGTGGCGCCATCACCAGTAATTCGG Majority
10 20 30 40 50
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1 TCCACATCGGTCCAATTAACATATGACGTGGCGCCATCACCAGTAATTCGG a909_al2.seq
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60 70 80 90 100
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101 AATATAGTCTTCTTGACTTAACAAACGTAAACGACCTTCATGGTAATCTC cohl_al2.seq
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TCTGCATTCTTGTATTAGTCATAAGATGCAGAAGGTGTAATTTTATACCC Majority
160 170 180 190 200
151 TCTGCATTCTTGTATTAATCATAAGATGCAGAAGGTGTAATTTTATACCC cohl_al2.seq
151 TCTGCATTCTTGTATTAGTCATAAGATGCAGAAGGTGTAATTTTATACCC a909_al2.seq
TGAATATCATTATCCGTAACACATCGACGAACATTTTCCACCATCATATC Majority
210 220 230 240 250
201 TGAATATCATTATCCGTAACACATCGACGAACATTTTCCACCATCATATC cohl_al2.seq
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260 270 280 290 300
251 ATGTGTCTCCCCTGGGAGACCATTTATTAGGTGAGAAACGATTTCTACTT cohl_al2.seq
251 ATGTGTCTCCCCTGGGAGACCATTTATTAGGTGAGAAACGATTTCTACTT a909_al2.seq
TAGGAGCTAATTCTCGTATTCTCTTAACAGTTTTTTTGTAAAGGTCATAT Majority
310 320 330 340 350
301 TAGGAGCTAATTCTCGTACTCTCTTAACAGTTTTTTTGTAAAGGTCATAT cohl_al2.seq
301 TAGGAGCTAATTCTCGTATTCTCTTAACAGTTTTTTTGTAAAGGTCATAT a909_al2.seq
GAATGTGCTCTATTTATTAATGCAGAAGTTGCTTCATAAGTTGTCTGAAG Majority
360 370 380 390 400
351 GAATGTGCTCTATTTATTAATGCAGAAGTTGCTTCATAAGTTGTCTGAAG cohl_al2.seq
351 GAATGTGCTCTATTTATTAATGCAGAAGTTGCTTCATAAGTTGTCTGAAG a909_al2.seq
GCCTAATTCTAAAGTCACATGCATTCTTTCAGAAAGTTCAGCGAGATAGT Majority
410 420 430 440 450
401 GCCTAATTCTAAAGTCACATGCATTCTTTCAGAAAGTTCAGCGAGATAGT cohl_al2.seq
401 GCCTAATTCTAAAGTCACATGCATTCTTTCAGAAAGTTCAGCGAGATAGT a909_al2.seq
ATATAGTTTCATCAGGTAAGCAATCCGGCCTTGTTCCGATGTTGATCCCG Majority
460 470 480 490 500
451 ATATAGTTTCATCAGGTAAGCAATCCGGCCTTGTTCCGATGTTGATCCCG cohl_al2.seq
451 ATATAGTTTCATCAGGTAAGCAATCCGGCCTTGTTCCGATGTTGATCCCG a909_al2.seq
ATAACTCCTGGCTCATTAATAGCCTGTTCGTAACGCTCTTTAATTATCTC Majority
510 520 530 540 550
501 ATAACTCCTGGCTCATTAATAGCCTGTTCGTAACGCTCTTTAATTATCTC cohl_al2.seq
501 ATAACTCCTGGCTCATTAATAGCCTGTTCGTAACGCTCTTTAATTATCTC a909_al2.seq
TAACTTAGCATGGGTATTGGTAAAATTTTGAAAATAGACTAAGTATTTAT Majority
560 570 580 590 600
551 TAACTTAGCATGGGTATTGGTAAAATTTTGAAAATAGACTAAGTATTTAT cohl_al2.seq
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TAACCTCAGGCCACTTTCTATGCATGAAATCAATTTCTTTATAGAATTGT Majority
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601 TAACCTCAGGCCACTTTCTATGCATGAAATCAATTTCTTTATAGAATTGT cohl_al2.seq
601 TAACCTCAGGCCACTTTCTATGCATGAAATCAATTTCTTTATAGAATTGT a909_al2.seq

Figure 21

```
TCACGAATAGGAGCTTCTGGAGCAACTATAGCATCCCCTGAACCAGAAAC Majority
          660       670       680       690       700
651 TCACGAATAGGAGCTTCTGGAGCAACTATAGCATCCCCTGAACCAGAAAC cohl_al2.seq
651 TCACGAATAGGAGCTTCTGGAGCAACTATAGCATCCCCTGAACCAGAAAC a909_al2.seq

TGTGCAAAAAGTGCACCCTCCTCTAGCAACTGTTCCATCTCTGTTAGGAC Majority
          710       720       730       740       750
701 TGTGCAAAAAGTGCACCCTCCTCTAGCAACTGTTCCATCTCTGTTAGGAC cohl_al2.seq
701 TGTGCAAAAAGTGCACCCTCCTCTAGCAACTGTTCCATCTCTGTTAGGAC a909_al2.seq

AGTCAAAACCAGCATCTATAGGTAATTTAAATATTTTTTCTCCAAAGAGT Majority
          760       770       780       790       800
751 AGTCAAAACCAGCATCTATAGGTAATTTAAATATTTTTTCTCCAAAGAGT cohl_al2.seq
751 AGTCAAAACCAGCATCTATAGGTAATTTAAATATTTTTTCTCCAAAGAGT a909_al2.seq

TCTCGATAATAATCATTAATCGCACGATAACGTTTTTTTCATAGGATAATT Majority
          810       820       830       840       850
801 TCTCGATAATAATCATTAATCGCACGATAACGTTTTTTTCATAGGATAATT cohl_al2.seq
801 TCTCGATAATAATCATTAATCGCACGATAACGTTTTTTTCATAGGATAATT a909_al2.seq

GTATCACAATTTTAACTAAAATAACCTCACTACTACAATAAAACTAAAAA Majority
          860       870       880       890       900
851 GTATCACAATTTTAACTAAAATAACCTCACTACTACAATAAAACTAAAAA cohl_al2.seq
851 GTATCACAATTTTAACTAAAATAACCTCACTACTACAATAAAACTAAAAA a909_al2.seq

AGATTGGAACGTCAGTTAGTTCCAATCTTTTATTTACTTCACTTTCTTTA Majority
          910       920       930       940       950
901 AGATTGGAACGTCAGTTAGTCCCAATCTTTTATTTACTTCACTTTCTTTA cohl_al2.seq
901 AGATTGGAACGTCAGTTAGTTCCAATCTTTTATTTACTTCACTTTCTTTA a909_al2.seq

ACCAATCCTTGGCTAAAAAGATATACGCAGTTAGATTCAAAATACCATAA Majority
          960       970       980       990      1000
951 ACCAATCCTTGGATAAAAAGATATACGCAGTTAGATTCAAAATACCATAA cohl_al2.seq
951 ACCAATCCTTGGCTAAAAAGATATACGCAGTTAGATTCAAAATACCATAA a909_al2.seq

GCAAGTATAAAACCAGCTAAAACATCTGTCGGAAAATGAACCCCTAGGTA Majority
         1010      1020      1030      1040      1050
1001 GCAAGTATAAAACCAGCTAAAACATCTGTCGGAAAATGAACCCCTAGGTA cohl_al2.seq
1001 GCAAGTATAAAACCAGCTAAAACATCTGTCGGAAAATGAACCCCTAGGTA a909_al2.seq

AATACGAGATAACCCAATTAAAAAAATGAGCAAACCCAATGTACCTTGGC Majority
         1060      1070      1080      1090      1100
1051 AATACGAGATAACCCAATTAAAAAAATGAGCAAACCCAATGTACCTTGGC cohl_al2.seq
1051 AATACGAGATAACCCAATTAAAAAAATGAGCAAACCCAAAATACCTTGGC a909_al2.seq

ACAACAGTTTCCATATACTCTTAGGCATATAGTACTGCAATAAAATAATA Majority
         1110      1120      1130      1140      1150
1101 ACAACAGTTTCCATATACTCTTAGGCATATAGTACTGCAATAAAATAATA cohl_al2.seq
1101 ACAACAGTTTCCATATACTCTTAGGCATATAGTACTGCAATAAAATAATA a909_al2.seq

CTACTCCCAAATATCATAAATGTTCCCATCGAGTGCCCACTGGGAAACGA Majority
         1160      1170      1180      1190      1200
1151 CTACTCCCAAATATCATAAATGTTCCCATCGAGTGCCCACTGGGAAACGA cohl_al2.seq
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ATAGCCACCTGCAAATACTAAATGGGTTAAAGTTGGTCTCACTCTTTGAA Majority
         1210      1220      1230      1240      1250
1201 ATAGCCACCTGCAAATACTAAATGGGTTAAAGTTGGTCTCACTCTTTGAA cohl_al2.seq
1201 ATAGCCACCTGCAAATACTAAATGGGTTAAAGTTGGTCTCACTCTTTGAA a909_al2.seq

AAATAAGTTTTAAAGAAAGTATACATATACCAGAGATAATAGCATTTACT Majority
         1260      1270      1280      1290      1300
1251 AAATAAGTTTTAAAGAAAGTATACATATACCAGAGATAATAGCATTTACT cohl_al2.seq
1251 AAATAAGTTTTAAAGAAAGTATACATATACCAGAGATAATAGCATTTACT a909_al2.seq
```

FIGURE 21A

```
GCGATAAATCTAGCTTGAGGATACCACTTCTTAAGGTAACAGAAAGTGAC Majority
        1310        1320        1330        1340        1350
1301 GCGATAAATCTAGCTTGAGGATACCACTTCTTAAGGTAACAGAAAGTGAC cohl_a12.seq
1301 GCGATAAATCTAGCTTGAGGATACCACTTCTTAAGGTAACAGAAAGTGAC a909_a12.seq

GCTCATAATCGCAATAGCTATCTGGCTTACAGTATTACCAACCACAGTGA Majority
        1360        1370        1380        1390        1400
1351 GCTCATAATCGCAATAGCTATCTGGCTTACAGTATTACCAACCACAGTGA cohl_a12.seq
1351 GCTCATAATCGCAATAGCTATCTGGCTTACAGTATTACCAACCACAGTGA a909_a12.seq

TTAACTTGAAAAATCTTGTAGAAAGATTTGGCAACTGTCCTCTAACACTT Majority
        1410        1420        1430        1440        1450
1401 TTAACTTAAAAAATCTTGTAGAAAGATTTGGCAACTGTCCTCTAACACTT cohl_a12.seq
1401 TTAACTTGAAAAATCTTGTAGAAAGATTTGGCAACTGTCCTCTAACACTT a909_a12.seq

TCTTGAATAGTTTGGTCAAATGCGATTACAGTGTCGGGCCAATATTTGAT Majority
        1460        1470        1480        1490        1500
1451 TCTTGAATAGTTTGGTCAAATGCGATTACAGTGTCGGGCCAATATTTGAT cohl_a12.seq
1451 TCTTGAATAGTTTGGTCAAATGCGATTACAGTGTCGGGCCAATATTTGAT a909_a12.seq

GACCAATCCTAAACTGAAAAATAAGATAATAGCAATAAATGCTTGAATAA Majority
        1510        1520        1530        1540        1550
1501 GACCAATCCTAAACTGAAAAATAAGATAATAGCAATAAATGCTTGAATAA cohl_a12.seq
1501 GACCAATCCTAAACTGAAAAATAAGATAATAGCAATAAATGCTTGAATAA a909_a12.seq

GTTTACTATTTTGACGAGATAAGATTAGTCTTTTTATATCTTTCTAATAT Majority
        1560        1570        1580        1590        1600
1551 GTTTACTATTTTGACGAGATAACATTAGTCTTTTTATATCTTTCTAATAT cohl_a12.seq
1551 GTTTACTATTTTGACGAGATAACATTAGTCTTTTTATATCTTTCTAATAT a909_a12.seq

TGGCAAACAAGCCACGTAAGTTAGATAGAAAACAATCGAAATTAAAATTC Majority
        1610        1620        1630        1640        1650
1601 TGGCAAACAAGCCACGTAAGTTAGATAGAAAACAATCGAAATTAAAATTC cohl_a12.seq
1601 TGGCAAACAAGCCACGTAAGTTAGATAGAAAACAATCGAAATTAAAATTC a909_a12.seq

CCTCAACGATATTAAATGGAATAACCATTGTTAAAAGGTAATTGCCTACA Majority
        1660        1670        1680        1690        1700
1651 CCTCAACGATATTAAATGGAATAACCATTGTTAAAAGGTAATTGCCTACA cohl_a12.seq
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CCAATAAATGTTCTGATATCAAAGTTAGCAAATATAGCATACAAAGGAAT Majority
        1710        1720        1730        1740        1750
1701 CCAATAAATGTTCTGATATCAAAGTTAGCAAATATAGCATACAAAGGAAT cohl_a12.seq
1701 CCAATAAATGTTCTGATATCAAAGTTAGCAAATATAGCATACAAAGGAAT a909_a12.seq

CGCAAAGACATAGTTGAGAGCTACCATAGATACAGTCAAGCTAACTGTAC Majority
        1760        1770        1780        1790        1800
1751 CGCAAAGACATAGTTGAGAGCTACCATAGATACAGTCAAGCTAACTGTAC cohl_a12.seq
1751 CGCAAAGACATAGTTGAGAGCTACCATAGATACAGTCAAGCTAACTGTAC a909_a12.seq

CAAATAAACTAGCTTTAATAAAATCTTTTGCACTCTCTCTATTTTTCCAG Majority
        1810        1820        1830        1840        1850
1801 CAAATAAACTAGCTTTAATAAAATCTTTTGCACTCTCTCTATTTTTCCAG cohl_a12.seq
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AAAATAGCGAAACTTGCTAAAAATAGAGCTAGAGCAACCATATTCATCGG Majority
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        1910        1920        1930        1940        1950
1901 TAAACCGATAAAGGTTTCTGGACCACGATTAGCAAGTATAACTTTTAAAA cohl_a12.seq
1901 TAAACCGATAAAGGTTTCTGGACCACGATTAGCAAGTATAACTTTTAAAA a909_a12.seq
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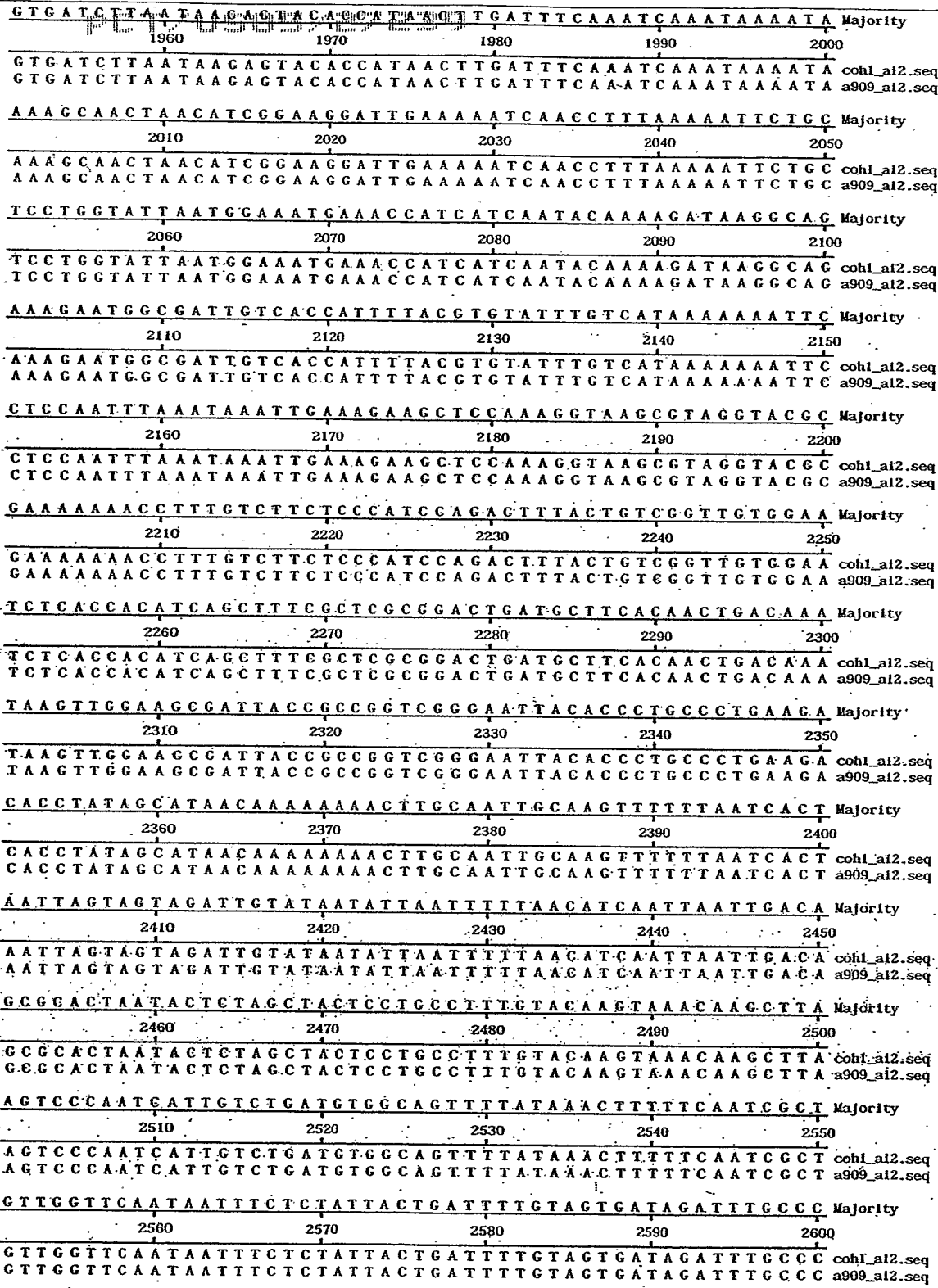
FIGURE 21B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1951 GTGATCTTAATAAGAGTACACCATAACTTGATTTCAAATCAAATAAAATA cohl_al2.seq
1951 GTGATCTTAATAAGAGTACACCATAACTTGATTTCAAATCAAATAAAATA a909_al2.seq
AAAGCAACTAACATCGGAAGGATTGAAAAATCAACCTTTAAAAATTCTGC Majority
2010 2020 2030 2040 2050
2001 AAAGCAACTAACATCGGAAGGATTGAAAAATCAACCTTTAAAAATTCTGC cohl_al2.seq
2001 AAAGCAACTAACATCGGAAGGATTGAAAAATCAACCTTTAAAAATTCTGC a909_al2.seq
TCCTGGTATTAATGGAAATGAAACCATCATCAATACAAAAGATAAGGCAG Majority
2060 2070 2080 2090 2100
2051 TCCTGGTATTAATGGAAATGAAACCATCATCAATACAAAAGATAAGGCAG cohl_al2.seq
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AAAGAATGGCGATTGTCACCATTTTACGTGTATTTGTCATAAAAAAAATTC Majority
2110 2120 2130 2140 2150
2101 AAAGAATGGCGATTGTCACCATTTTACGTGTATTTGTCATAAAAAAAATTC cohl_al2.seq
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CTCCAATTTAAATAAATTGAAAGAAGCTCCAAAGGTAAGCGTAGGTACGC Majority
2160 2170 2180 2190 2200
2151 CTCCAATTTAAATAAATTGAAAGAAGCTCCAAAGGTAAGCGTAGGTACGC cohl_al2.seq
2151 CTCCAATTTAAATAAATTGAAAGAAGCTCCAAAGGTAAGCGTAGGTACGC a909_al2.seq
GAAAAAAAACCTTTGTCTTCTCCCATCCAGACTTTACTGTCGGTTGTGGAA Majority
2210 2220 2230 2240 2250
2201 GAAAAAAAACCTTTGTCTTCTCCCATCCAGACTTTACTGTCGGTTGTGGAA cohl_al2.seq
2201 GAAAAAAAACCTTTGTCTTCTCCCATCCAGACTTTACTGTCGGTTGTGGAA a909_al2.seq
TCTCACCACATCAGCTTTCGCTCGCGGACTGATGCTTCACAACTGACAAA Majority
2260 2270 2280 2290 2300
2251 TCTCACCACATCAGCTTTCGCTCGCGGACTGATGCTTCACAACTGACAAA cohl_al2.seq
2251 TCTCACCACATCAGCTTTCGCTCGCGGACTGATGCTTCACAACTGACAAA a909_al2.seq
TAAGTTGGAAGCGATTACCGCCGGTCGGGAATTACACCCTGCCCTGAAGA Majority
2310 2320 2330 2340 2350
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CACCTATAGCATAACAAAAAAAAACTTGCAATTGCAAGTTTTTTAATCACT Majority
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GTTGGTTCAATAATTTCTCTATTACTGATTTTGTAGTGATAGATTTGCCC Majority
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2551 GTTGGTTCAATAATTTCTCTATTACTGATTTTGTAGTGATAGATTTGCCC cohl_al2.seq
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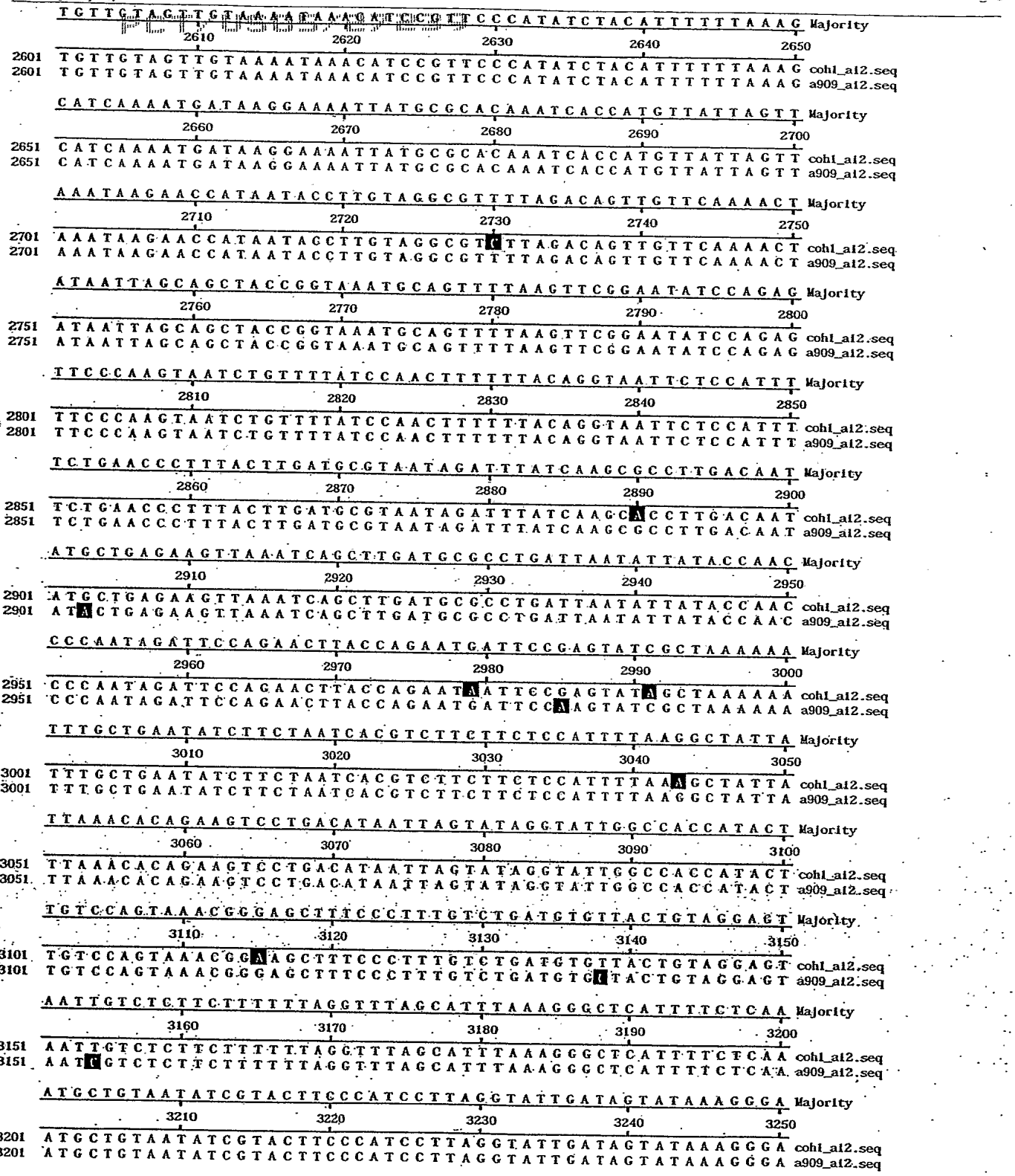
FIGURE 21C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CATCAAAATGATAAGGAAAATTATGCGCACAAATCACCATGTTATTAGTT Majority
2660 2670 2680 2690 2700
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2801 TTCCCAAGTAATCTGTTTTATCCAACTTTTTTACAGGTAATTCTCCATTT a909_al2.seq
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2851 TCTGAACCCTTTACTTGATGCGTAATAGATTTATCAAGCACCTTGACAAT cohl_al2.seq
2851 TCTGAACCCTTTACTTGATGCGTAATAGATTTATCAAGCGCCTTGACAAT a909_al2.seq
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2910 2920 2930 2940 2950
2901 ATGCTGAGAAGTTAAATCAGCTTGATGCGCCTGATTAATATTATACCAAC cohl_al2.seq
2901 ATACTGAGAAGTTAAATCAGCTTGATGCGCCTGATTAATATTATACCAAC a909_al2.seq
CCCAATAGATTCCAGAACTTACCAGAATGATTCCGAGTATCGCTAAAAAA Majority
2960 2970 2980 2990 3000
2951 CCCAATAGATTCCAGAACTTACCAGAATAATTCCGAGTATAGCTAAAAAA cohl_al2.seq
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TTTGCTGAATATCTTCTAATCACGTCTTCTTCTCCATTTTAAGGCTATTA Majority
3010 3020 3030 3040 3050
3001 TTTGCTGAATATCTTCTAATCACGTCTTCTTCTCCATTTTAAAGCTATTA cohl_al2.seq
3001 TTTGCTGAATATCTTCTAATCACGTCTTCTTCTCCATTTTAAGGCTATTA a909_al2.seq
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3051 TTAAACACAGAAGTCCTGACATAATTAGTATAGGTATTGGCCACCATACT cohl_al2.seq
3051 TTAAACACAGAAGTCCTGACATAATTAGTATAGGTATTGGCCACCATACT a909_al2.seq
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3101 TGTCCAGTAAACGGAAGCTTTCCCTTTGTCTGATGTGTTACTGTAGGAGT cohl_al2.seq
3101 TGTCCAGTAAACGGGAGCTTTCCCTTTGTCTGATGTGCTACTGTAGGAGT a909_al2.seq
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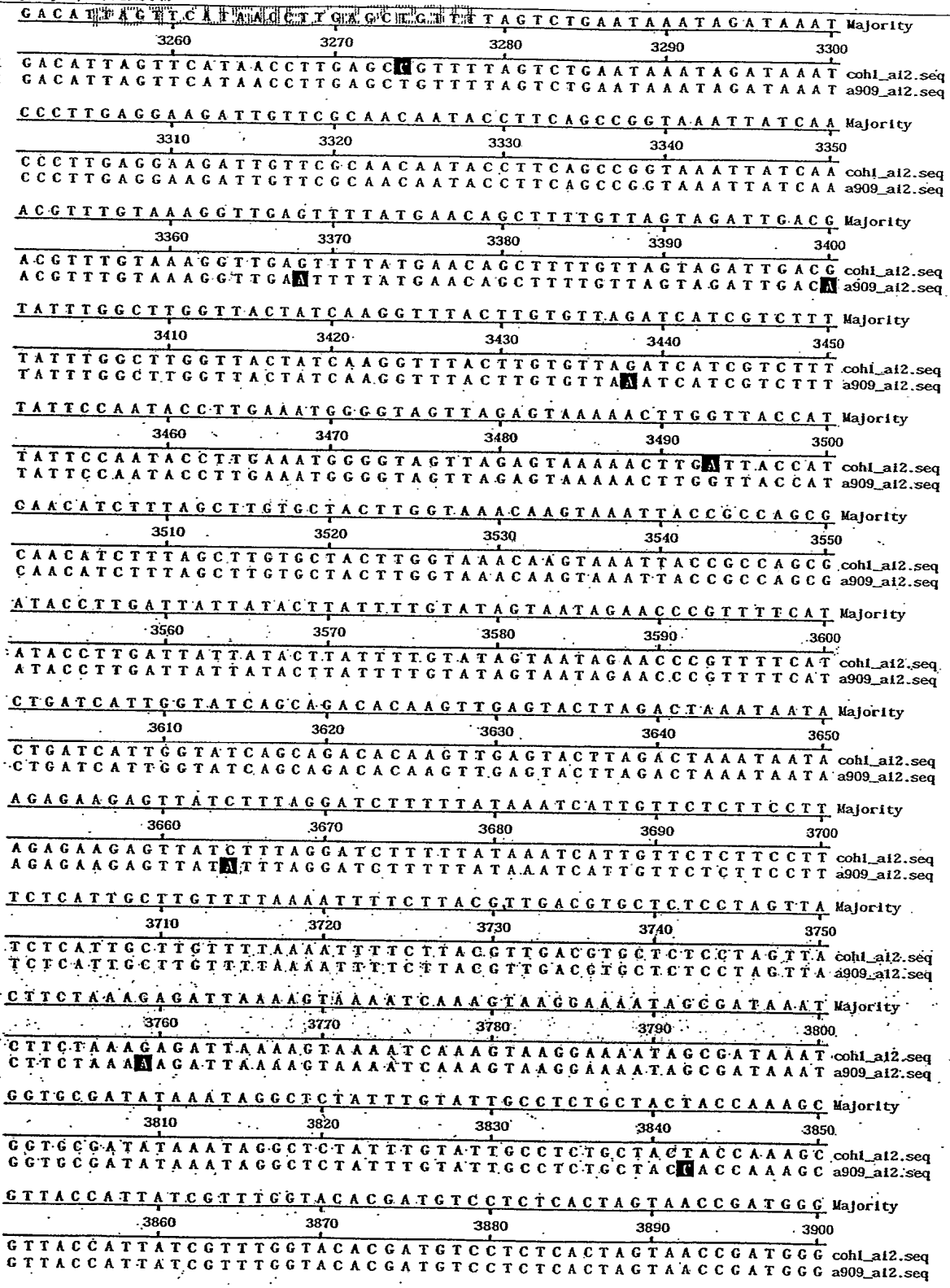
FIGURE 21D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3360 3370 3380 3390 3400
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3460 3470 3480 3490 3500
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3560 3570 3580 3590 3600
3551 ATACCTTGATTATTATACTTATTTTGTATAGTAATAGAACCCGTTTTCAT cohl_al2.seq
3551 ATACCTTGATTATTATACTTATTTTGTATAGTAATAGAACCCGTTTTCAT a909_al2.seq
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3610 3620 3630 3640 3650
3601 CTGATCATTGGTATCAGCAGACACAAGTTGAGTACTTAGACTAAATAATA cohl_al2.seq
3601 CTGATCATTGGTATCAGCAGACACAAGTTGAGTACTTAGACTAAATAATA a909_al2.seq
AGAGAAGAGTTATCTTTAGGATCTTTTTATAAATCATTGTTCTCTTCCTT Majority
3660 3670 3680 3690 3700
3651 AGAGAAGAGTTATCTTTAGGATCTTTTTATAAATCATTGTTCTCTTCCTT cohl_al2.seq
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TCTCATTGCTTGTTTTAAAATTTTCTTACGTTGACGTGCTCTCCTAGTTA Majority
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3701 TCTCATTGCTTGTTTTAAAATTTTCTTACGTTGACGTGCTCTCCTAGTTA cohl_al2.seq
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CTTCTAAAGAGATTAAAAGTAAAATCAAAGTAAGGAAAATAGCGATAAAT Majority
3760 3770 3780 3790 3800
3751 CTTCTAAAGAGATTAAAAGTAAAATCAAAGTAAGGAAAATAGCGATAAAT cohl_al2.seq
3751 CTTCTAAAAAGATTAAAAGTAAAATCAAAGTAAGGAAAATAGCGATAAAT a909_al2.seq
GGTGCGATATAAATAGGCTCTATTTGTATTGCCTCTGCTACTACCAAAGC Majority
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GTTACCATTATCGTTTGGTACACGATGTCCTCTCACTAGTAACCGATGGG Majority
3860 3870 3880 3890 3900
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FIGURE 21E


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3901 TATTAACGCCATATGGTGTACACGTCACCAAAGTTTGGTAGTCTTTACCT cohl_al2.seq
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TTAACAATTTGTAAATCCCTCAAATCATCCGGTTTAACTGTTCTGATTTG Majority
3960 3970 3980 3990 4000
3951 TTAACAATTTGTAAATCCCTCAAATCATCCGGTTTAACTGTTCTGATTTC cohl_al2.seq
3951 TTAACAATTTGTAAATCCCTCAAATCATCCGGTTTAACTGTTCTGATTTG a909_al2.seq
ATCCACTTGATAAGTATATGTTTCATTTAAGATACTGACTGTCCAGTGGT Majority
4010 4020 4030 4040 4050
4001 ATCCACTTGATAAGTATATGTTTCATTTAAGATACTGACTGTCCAGTGGT cohl_al2.seq
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4060 4070 4080 4090 4100
4051 CTCCAACTTTTAACTTATCCAAATCAGAAAAAAGCCTTGAAGAGGGTAAA cohl_al2.seq
4051 CTCCAGCTTTTAACTTATCCAAATCAGAAAAAAGCCTTGAAGAGGGTAAA a909_al2.seq
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4110 4120 4130 4140 4150
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4160 4170 4180 4190 4200
4151 ACTACTTCCTTCTAAATGACCAATAGAAGTTTGAAGCACTTTTTCACTTG cohl_al2.seq
4151 ACTACTTCCTTCTAAATGACCAATAGAAGTTTGAAGCACCTTTTTCACTTG a909_al2.seq
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4210 4220 4230 4240 4250
4201 TACCATGATAAAGTGGTAATTTTATGTTTATCTTTGGAATTGAAATATAA cohl_al2.seq
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4260 4270 4280 4290 4300
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CTCTTGGTTAGTCATGTGCCACTTCATTCCTGAAGTTTTAAATTGCTTAT Majority
4310 4320 4330 4340 4350
4301 CTCTTGGCTAGTCATGTGCCACTTCATTCCTGAAGTTTTAAATTGCTTAT cohl_al2.seq
4301 CTCTTGGTCAGTCATGTGCCACTTCATTCCTGAAGTTTTAAATTGCTTAT a909_al2.seq
TATATTCTTTGGCTCGGTTAATAATTTTTTTATAGTCGTTTTCATCCATA Majority
4360 4370 4380 4390 4400
4351 TATATTCTTTGGCTCGGTTAATAATTTTTTTATAATCGTTTTCATCCATA cohl_al2.seq
4351 TATATTCTTTGGCTCGGTTAATAATTTTTTTATAGTCGTTTTCATCCATA a909_al2.seq
TGCGTTACGCGGTCTTGGTAATCCATAATCGCTCGAGATTGGTGAAATGA Majority
4410 4420 4430 4440 4450
4401 TGCGTTACGCGGTCTTGGTAATCCATAATCGCTCGAGATTGGTGAAATGA cohl_al2.seq
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ATTCCAATAATTAGCAAGTGAAGGATAAGCCATTAAGCCTACCCCCACTG Majority
4460 4470 4480 4490 4500
4451 ATTCCAATAATTAGCAAGTGAAGGATAAGCCATTAAGCCTACCCCCACTG cohl_al2.seq
4451 ATTCCAATAATTAGCAAGTGAAGGATAAGCCATTAAGCCTACCCCCACTG a909_al2.seq
CAATTATAGTGACAAGCAAAATGGATACTAAATGTTGTCTTATTTTTTTC Majority
4510 4520 4530 4540 4550
4501 CAATTATAGTGACAAGCAAAATGGATACTAAATGTTGTCTTATTTTTTTC cohl_al2.seq
4501 CAATTATAGTGACAAGCAAAATGGATACTAAATGTTGTCTTATTTTTTTC a909_al2.seq

FIGURE 21F

```
     ATATATTTTAAATCTGTACCACTTTGCTAGCCCATCTTATTAAGAACGTA Majority
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4551 ATATATTTTAAATCTGTACCACTTTGCTAGCCCATCTTATTAAGAACGTA a909_a12.seq

     AACGACGACGAGCAACAAGCACGATACCTGCTCCTATTACTAAAATTGCA Majority
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4601 AACGACGACGAGCAACAAGCACGATACCTGCTCCTATTACTAAAATTGCA a909_a12.seq

     CCTATAATGTAGAAAATTGTTGTACCAATACCACCTGTTGAAGGCAACTC Majority
              4660      4670      4680      4690      4700
4651 CCTATAATGTAGAAAATTGTTGTACCAATACCACCTGTTGAAGGCAACTC coh1_a12.seq
4651 CCTATAATGTAGAAAATTGTTGTACCAATACCACCTGTTGAAGGCAACTC a909_a12.seq

     AGTACCTTTGTTATTTTCAACAGTTGGGTTAACTAAAAGGTTATCTGAAT Majority
              4710      4720      4730      4740      4750
4701 AGTACCTTTGTTATTTTCAACAGTTGGGTTAACTAAAAGGTTATCTGAAT coh1_a12.seq
4701 AGTACCTTTGTTATTTTCAACAGTTGGGTTAACTAAAAGGTTATCTGAAT a909_a12.seq

     TAGTCGTATCAGTGGCTCCATCTCCTAAAATAACCTTCTGAGAGTTATCT Majority
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     TTCTTTCAAGCCTGTAATGGTAATTATACCATCTGCTCCTGTTGTATATT Majority
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5001 TGAAGCTTTTGTGGAACCATCAATTTTTTTTATAGTAATTTGACCATCCC coh1_a12.seq
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              5060      5070      5080      5090      5100
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     ACTCTTTAATACTCCTGTATAAGTGACTGTGATTGTATTTATTCCCTTAT Majority
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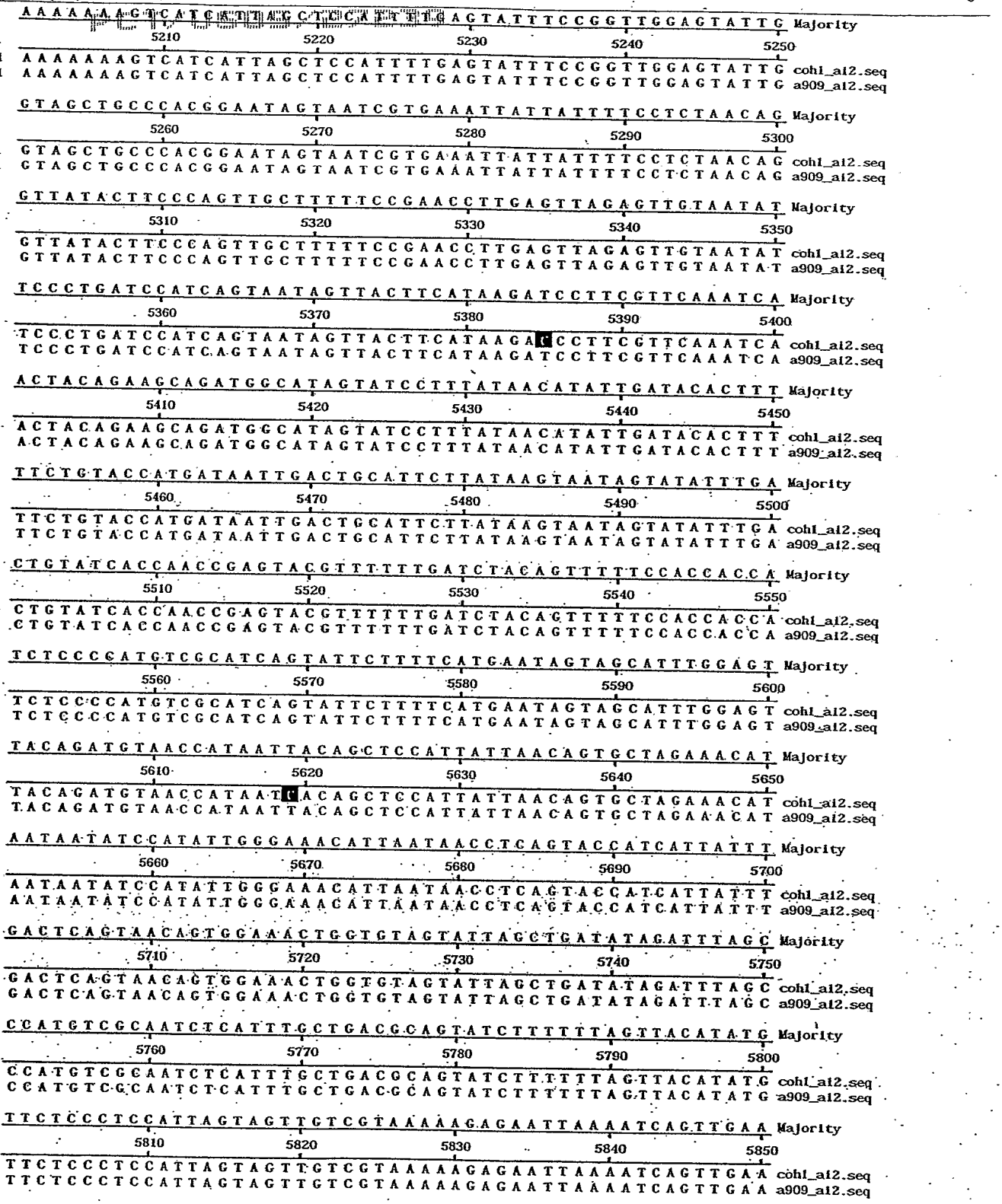
FIGURE 21G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GTAGCTGCCCACGGAATAGTAATCGTGAAATTATTATTTTCCTCTAACAG Majority
5260 5270 5280 5290 5300
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GTTATACTTCCCAGTTGCTTTTTCCGAACCTTGAGTTAGAGTTGTAATAT Majority
5310 5320 5330 5340 5350
5301 GTTATACTTCCCAGTTGCTTTTTCCGAACCTTGAGTTAGAGTTGTAATAT cohl_al2.seq
5301 GTTATACTTCCCAGTTGCTTTTTCCGAACCTTGAGTTAGAGTTGTAATAT a909_al2.seq
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5660 5670 5680 5690 5700
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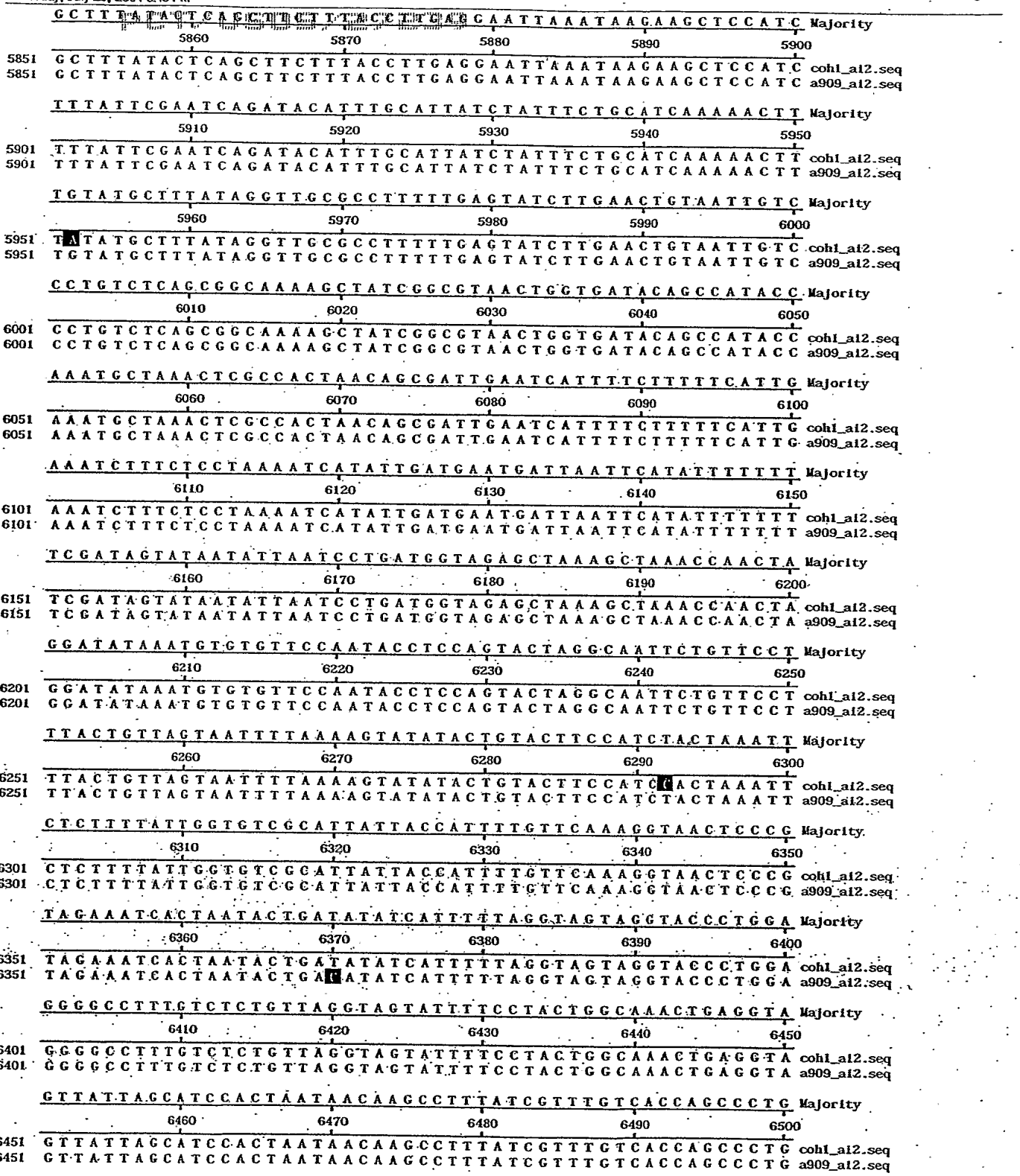
FIGURE 21H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TTTATTCGAATCAGATACATTTGCATTATCTATTTCTGCATCAAAAACTT Majority
5910 5920 5930 5940 5950
5901 TTTATTCGAATCAGATACATTTGCATTATCTATTTCTGCATCAAAAACTT cohl_al2.seq
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6201 GGATATAAATGTGTGTTCCAATACCTCCAGTACTAGGCAATTCTGTTCCT cohl_al2.seq
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6410 6420 6430 6440 6450
6401 GGGGCCTTTGTCTCTGTTAGGTAGTATTTTCCTACTGGCAAACTGAGGTA cohl_al2.seq
6401 GGGGCCTTTGTCTCTGTTAGGTAGTATTTTCCTACTGGCAAACTGAGGTA a909_al2.seq
GTTATTAGCATCCACTAATAACAAGCCTTTATCGTTTGTCACCAGCCCTG Majority
6460 6470 6480 6490 6500
6451 GTTATTAGCATCCACTAATAACAAGCCTTTATCGTTTGTCACCAGCCCTG cohl_al2.seq
6451 GTTATTAGCATCCACTAATAACAAGCCTTTATCGTTTGTCACCAGCCCTG a909_al2.seq

FIGURE 21I

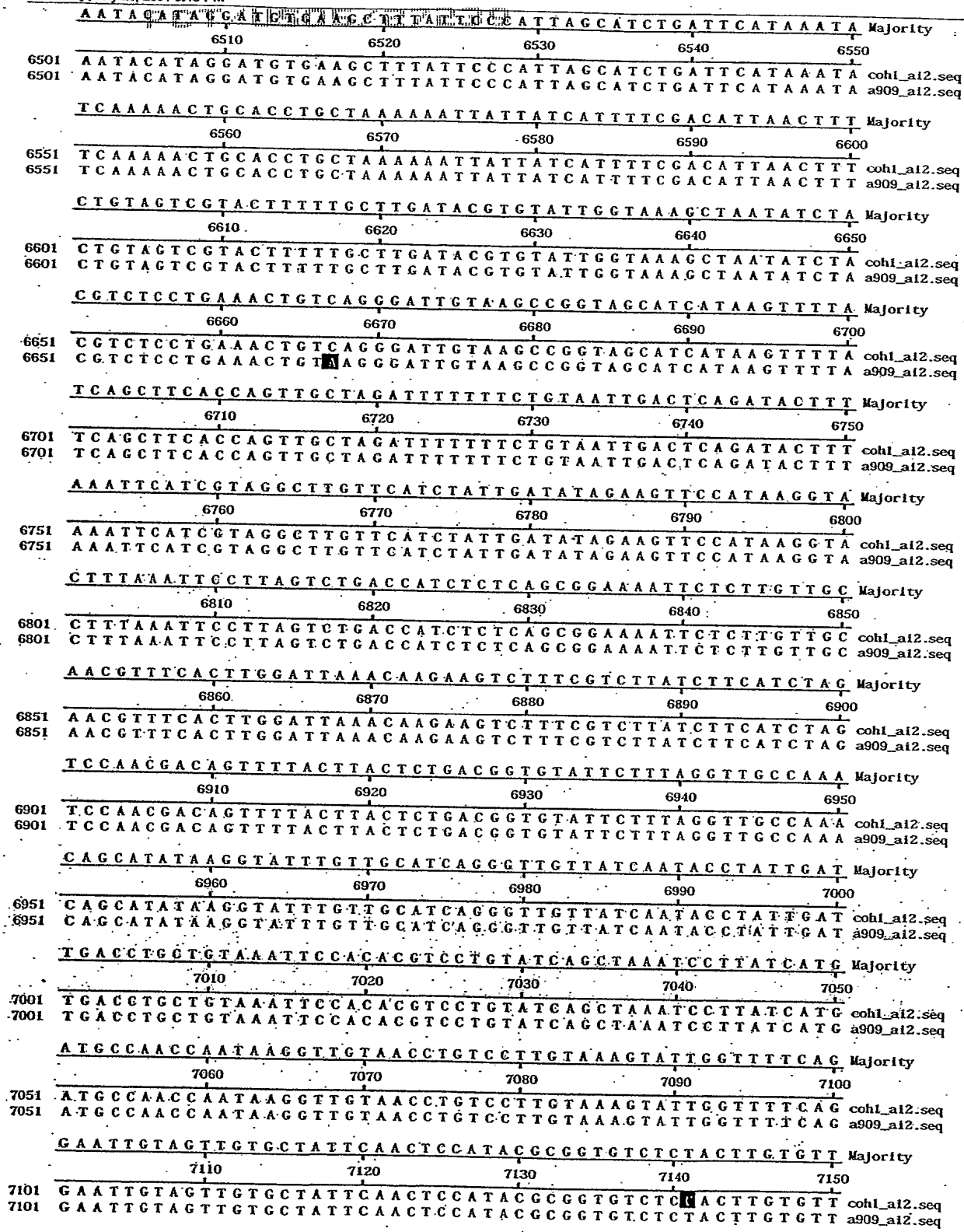
AATACATAGCATCTGAAGCTTTATTCCCATTAGCATCTGATTCATAAATA Majority
6510 6520 6530 6540 6550
6501 AATACATAGGATGTGAAGCTTTATTCCCATTAGCATCTGATTCATAAATA cohl_al2.seq
6501 AATACATAGGATGTGAAGCTTTATTCCCATTAGCATCTGATTCATAAATA a909_al2.seq
TCAAAAACTGCACCTGCTAAAAAATTATTATCATTTTCGACATTAACTTT Majority
6560 6570 6580 6590 6600
6551 TCAAAAACTGCACCTGCTAAAAAATTATTATCATTTTCGACATTAACTTT cohl_al2.seq
6551 TCAAAAACTGCACCTGCTAAAAAATTATTATCATTTTCGACATTAACTTT a909_al2.seq
CTGTAGTCGTACTTTTTGCTTGATACGTGTATTGGTAAAGCTAATATCTA Majority
6610 6620 6630 6640 6650
6601 CTGTAGTCGTACTTTTTGCTTGATACGTGTATTGGTAAAGCTAATATCTA cohl_al2.seq
6601 CTGTAGTCGTACTTTTTGCTTGATACGTGTATTGGTAAAGCTAATATCTA a909_al2.seq
CGTCTCCTGAAACTGTCAGGGATTGTAAGCCGGTAGCATCATAAGTTTTA Majority
6660 6670 6680 6690 6700
6651 CGTCTCCTGAAACTGTCAGGGATTGTAAGCCGGTAGCATCATAAGTTTTA cohl_al2.seq
6651 CGTCTCCTGAAACTGTAAGGGATTGTAAGCCGGTAGCATCATAAGTTTTA a909_al2.seq
TCAGCTTCACCAGTTGCTAGATTTTTTTCTGTAATTGACTCAGATACTTT Majority
6710 6720 6730 6740 6750
6701 TCAGCTTCACCAGTTGCTAGATTTTTTTCTGTAATTGACTCAGATACTTT cohl_al2.seq
6701 TCAGCTTCACCAGTTGCTAGATTTTTTTCTGTAATTGACTCAGATACTTT a909_al2.seq
AAATTCATCGTAGGCTTGTTCATCTATTGATATAGAAGTTCCATAAGGTA Majority
6760 6770 6780 6790 6800
6751 AAATTCATCGTAGGCTTGTTCATCTATTGATATAGAAGTTCCATAAGGTA cohl_al2.seq
6751 AAATTCATCGTAGGCTTGTTCATCTATTGATATAGAAGTTCCATAAGGTA a909_al2.seq
CTTTAAATTGCTTAGTCTGACCATCTCTCAGCGGAAAATTCTCTTGTTGC Majority
6810 6820 6830 6840 6850
6801 CTTTAAATTCCTTAGTCTGACCATCTCTCAGCGGAAAATTCTCTTGTTGC cohl_al2.seq
6801 CTTTAAATTCCTTAGTCTGACCATCTCTCAGCGGAAAATTCTCTTGTTGC a909_al2.seq
AACGTTTCACTTGGATTAAACAAGAAGTCTTTCGTCTTATCTTCATCTAG Majority
6860 6870 6880 6890 6900
6851 AACGTTTCACTTGGATTAAACAAGAAGTCTTTCGTCTTATCTTCATCTAG cohl_al2.seq
6851 AACGTTTCACTTGGATTAAACAAGAAGTCTTTCGTCTTATCTTCATCTAG a909_al2.seq
TCCAACGACAGTTTTACTTACTCTGACGGTGTATTCTTTAGGTTGCCAAA Majority
6910 6920 6930 6940 6950
6901 TCCAACGACAGTTTTACTTACTCTGACGGTGTATTCTTTAGGTTGCCAAA cohl_al2.seq
6901 TCCAACGACAGTTTTACTTACTCTGACGGTGTATTCTTTAGGTTGCCAAA a909_al2.seq
CAGCATATAAGGTATTTGTTGCATCAGGGTTGTTATCAATACCTATTGAT Majority
6960 6970 6980 6990 7000
6951 CAGCATATAAGGTATTTGTTGCATCAGGGTTGTTATCAATACCTATTGAT cohl_al2.seq
6951 CAGCATATAAGGTATTTGTTGCATCAGGGTTGTTATCAATACCTATTGAT a909_al2.seq
TGACCTGCTGTAAATTCCACACGTCCTGTATCAGCTAAATCCTTATCATG Majority
7010 7020 7030 7040 7050
7001 TGACCTGCTGTAAATTCCACACGTCCTGTATCAGCTAAATCCTTATCATG cohl_al2.seq
7001 TGACCTGCTGTAAATTCCACACGTCCTGTATCAGCTAAATCCTTATCATG a909_al2.seq
ATGCCAACCAATAAGGTTGTAACCTGTCCTTGTAAAGTATTGGTTTTCAG Majority
7060 7070 7080 7090 7100
7051 ATGCCAACCAATAAGGTTGTAACCTGTCCTTGTAAAGTATTGGTTTTCAG cohl_al2.seq
7051 ATGCCAACCAATAAGGTTGTAACCTGTCCTTGTAAAGTATTGGTTTTCAG a909_al2.seq
GAATTGTAGTTGTGCTATTCAACTCCATACGCGGTGTCTCTACTTGTGTT Majority
7110 7120 7130 7140 7150
7101 GAATTGTAGTTGTGCTATTCAACTCCATACGCGGTGTCTCTACTTGTGTT cohl_al2.seq
7101 GAATTGTAGTTGTGCTATTCAACTCCATACGCGGTGTCTCTACTTGTGTT a909_al2.seq

FIGURE 21J